

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:24:31 ; Search time 138.696 Seconds
(without alignments)
81.226 Million cell updates/sec

Title: US-09-462-909D-9
Perfect score: 59
Sequence: 1 XXXXXWSXXXCSXXCGXXXXX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	41	69.5	504	Q69HL7	Q69hl7 ciona intes
2	41	69.5	3869	Q86PQ3	Q86pq3 cryptospori
3	40	67.8	59	Q7KYY3	Q7ky3 homo sapien
4	40	67.8	238	Q76510	Q76510 cryptospori
5	40	67.8	238	Q69HT6	Q69ht6 ciona intes
6	40	67.8	257	Q966K7	Q966k7 caenorhabdi
7	40	67.8	478	Q8BVE5	Q8bve5 m mus muscu
8	40	67.8	632	Q6ZPQ8	Q6zpq8 mus musculu
9	40	67.8	872	Q22580	Q22580 caenorhabdi
10	40	67.8	1077	SM5A_MOUSE	Q62217 mus musculu
11	40	67.8	1088	Q6PCX8	Q6pck8 xenopus lae
12	40	67.8	1092	Q6UY12	Q6uy12 homo sapien
13	40	67.8	1093	SM5B_HUMAN	Q9p283 homo sapien
14	40	67.8	1093	SM5B_MOUSE	Q60519 mus musculu
15	40	67.8	1093	Q7QC32	Q7qc32 anopheles g
16	40	67.8	1107	Q8BHP3	Q8bhp3 mus musculu
17	40	67.8	1122	Q7TT33	Q7tt33 mus musculu
18	40	67.8	1151	Q6DD89	Q6dd89 homo sapien
19	40	67.8	1170	TSP1_HUMAN	P07996 homo sapien
20	40	67.8	1170	TSP1_MOUSE	P35441 mus musculu
21	40	67.8	1170	Q71SA3	Q71sa3 rattus norv
22	40	67.8	1171	Q80YQ1	Q80yq1 mus musculu
23	40	67.8	1171	Q8CGB2	Q8cgb2 mus musculu
24	40	67.8	1536	Q9C0I4	Q9c0i4 homo sapien
25	40	67.8	1607	Q6P4U0	Q6p4u0 mus musculu
26	40	67.8	4998	Q8CG65	Q8cg65 mus musculu
27	40	67.8	5141	Q700K0	Q700k0 rattus norv
28	39	66.1	106	Q43982	Q43982 cryptospori
29	39	66.1	156	Q8MXV6	Q8mxy6 cryptospori
30	39	66.1	168	Q9GZ21	Q9gz21 cryptospori
31	39	66.1	168	Q9GZ22	Q9gz22 cryptospori

32	39	66.1	168	2	Q9GZ23	Q9gz23 cryptospori
33	39	66.1	192	2	Q7JN23	Q7jn23 cryptospori
34	39	66.1	206	2	Q24927	Q24927 eimeria ten
35	39	66.1	449	2	Q8QFV1	Q8qfv1 xenopus lae
36	39	66.1	461	2	Q95S22	Q95s22 drosophila
37	39	66.1	549	2	Q8T988	Q8t988 drosophila
38	39	66.1	592	1	TOH2_CABEL	P98060 caenorhabdi
39	39	66.1	598	2	O02029	O02029 drosophila
40	39	66.1	601	2	Q9V746	Q9v746 drosophila
41	39	66.1	612	2	Q6ZQ96	Q6zq96 mus musculu
42	39	66.1	628	2	Q7KRF4	Q7krf4 drosophila
43	39	66.1	654	2	Q19284	Q19284 caenorhabdi
44	39	66.1	656	2	Q86PQ8	Q86pq8 cryptospori
45	39	66.1	660	2	Q23832	Q23832 cryptospori

ALIGNMENTS

RESULT 1
Q69HL7 ID Q69HL7 PRELIMINARY; PRT; 504 AA.
AC Q69HL7; 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE HRTT-1-like (Fragment).
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23047825; PubMed=14686582;
RA Terajima D., Yamada S., Uchino R., Ikawa S., Ikeda M., Shida K.,
RA Arai Y., Wang H.G., Satoh N., Satake M.;
RT "Identification and sequence of seventy-nine new transcripts expressed
RT in hemocytes of Ciona intestinalis, three of which may be involved in
RT characteristic cell-cell communication.";
RL DNA Res. 10:203-212(2003).
DR EMBL; AY261898; AAP91764.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002413; V5_allergen.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00090; TSP_1; 4.
DR PRINTS; PR00838; V5ALLERGEN.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS01009; CRISP_1; 1.
DR PROSITE; PS01010; CRISP_2; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS50092; TSP1; 5.
FT NON_TER 1
FT NON_TER 504
SQ SEQUENCE 504 AA; 55337 MW; 305F43A92B850F29 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 504;
Best Local Similarity 50.0%; Pred.No. 7.1;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
|||
Db 477 WSAWSACSTSCG 488

RESULT 2
Q86PQ3 ID Q86PQ3 PRELIMINARY; PRT; 3869 AA.

Fri Apr 1 15:03:07 2005

AC Q86PQ3; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TSP1 domain-containing protein TSP2 precursor.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22326344; PubMed=12438378;
RX DOI=10.1128/IAI.70.12.6987-6995.2002;
RA Deng M., Templeton T.J., London N.R., Bauer C., Schroeder A.A.,
RA Abrahamson M.S.;
RT "Cryptosporidium parvum genes containing thrombospondin type 1
domains";
RL Infect. Immun. 70:6987-6995(2002).
DR EMBL; AY190984; AAC039046.1; -.
DR HSSP; P07996; ILSL.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR002086; Aldehyd_dehydrog.
DR InterPro; IPR000800; Notch_region.
DR InterPro; IPR003582; ShKT.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00066; Notch; 2.
DR Pfam; PF01549; ShTK; 5.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00090; TSP_1; 10.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00004; NL; 6.
DR SMART; SM00254; ShKT; 5.
DR SMART; SM00209; TSP1; 11.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; UNKNOWN 3.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS50092; TSP1; 10.
KW Signal.
FT SIGNAL
SQ SEQUENCE 3869 AA; 429514 MW; 1F4851B7B0787B87 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 3869;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 386 WSSWSSCSTSCG 397

RESULT 3
Q7KY3
ID Q7KY3 PRELIMINARY; PRT; 59 AA.
AC Q7KY3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Thrombospondin-lp180 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dimitry J.M., Sheibani N., Finn M., Boak B.M., Paul L.L.,
RA Frazier W.A.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12471; AAA21127.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF00090; TSP_1; 1.

DR PRINTS; PR01705; TSP1REPEAT.
DR PROSITE; PS50092; TSP1; 1.
FT NON_TER 1
FT NON_TER 59
SQ SEQUENCE 59 AA; 6445 MW; C6409E62332708A4 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 59;
Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 22 WSEWTSCTSCG 33

RESULT 4
O76510 PRELIMINARY; PRT; 238 AA.
ID O76510
AC O76510;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C3;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoreDun;
RA Spano F., Putignani L., Crisanti A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF073838; AAC26812.1; -.
DR HSSP; P07996; ILSL.
DR InterPro; IPR002086; Aldehyd_dehydrog.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 3.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 238
SQ SEQUENCE 238 AA; 26307 MW; 28242DE88F62C5A2 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 238;
Best Local Similarity 50.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WXXXXXCSXXCG 17
Db 47 WSSWSACSKSCG 58

RESULT 5
Q69HT6
ID Q69HT6 PRELIMINARY; PRT; 238 AA.
AC Q69HT6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hemicentin-like (Fragment).
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23047825; PubMed=14686582;
RA Terajima D., Yamada S., Uchino R., Ikawa S., Ikeda M., Shida K.,
RA Arai Y., Wang H.G., Satoh N., Satake M.;
RT "Identification and sequence of seventy-nine new transcripts expressed
in hemocytes of Ciona intestinalis, three of which may be involved in

RT characteristic cell-cell communication.";
RL DNA Res. 10:203-212(2003).
DR EMBL; AY261829; AAP91695.1; --
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP 1; 4.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS50092; TSP1; 4.
FT NON TER 1
SQ SEQUENCE 238 AA; 25294 MW; 7C40DAD7D7C57932 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 238;
Best Local Similarity 50.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
|| || ||
Db 26 WSTFGVCSASCG 37

RESULT 6
Q966K7 PRELIMINARY; PRT; 257 AA.
AC Q966K7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein F14H12.3.
GN Name=F14H12.3; ORFNames=F14H12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Gattung S., R Wilson.;
RT "The sequence of C. elegans cosmid F14H12.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006630; AAK68325.1; --
DR HSSP; P07996; 1LSL.

DR WormBase; WBGene00017471; F14H12.3.
DR WormPep; F14H12.3; CE07063.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000885; TSP 1.
DR Pfam; PF00090; TSP 1; 3.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS50092; TSP1; 3.
KW Hypothetical protein.
SQ SEQUENCE 257 AA; 26512 MW; 9B052A0D07F2BEFF CRC64;

Query Match 67.8%; Score 40; DB 2; Length 257;
Best Local Similarity 50.0%; Pred. No. 6.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
|| || || ||
Db 145 WSSWSACSVTCG 156

RESULT 7
Q8BVE5 PRELIMINARY; PRT; 478 AA.
AC Q8BVE5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched
library, clone:7330442G16 product:sema domain, seven thrombospondin
repeats (type 1 and type 1-like), transmembrane domain (TM) and short
cytoplasmic domain, (semaphorin) 5B, full insert sequence.
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Fri Apr 1 15:03:07 2005

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RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK078659; BAC37350.1; -.
DR HSSP; P07996; 1LSL.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000885; TSP_1.
DR Pfam; PF00090; TSP_1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 5.
DR PROSITE; PS50092; TSP1; 5.
DR Transmembrane.
KW NON TER 1
FT SEQUENCE 478 AA; 51394 MW; F4A9DFF173FOA376 CRC64;
SQ
Query Match 67.8%; Score 40; DB 2; Length 478;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXXCSXXCG 17
Db 19 WSSWAQCSTSCG 30

RESULT 8
Q6ZPQ8 Q6ZPQ8 PRELIMINARY; PRT; 632 AA.
AC Q6ZPQ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA1445 protein (Fragment).
GN Name=MKIAA1445;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT III. the complete nucleotide sequences of 500 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129362; BAC98172.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003659; Plexin-like.

InterPro; IPR002165; Plexin_repeat.
InterPro; IPR000884; TSP1.
InterPro; IPR000885; TSP_1.
Pfam; PF01437; PSI; 1.
Pfam; PF00090; TSP_1; 5.
PRINTS; PR01705; TSP1REPEAT.
SMART; SM00423; PSI; 1.
SMART; SM00209; TSP1; 5.
PROSITE; PS50092; TSP1; 5.
NON TER 1
SEQUENCE 632 AA; 69037 MW; 78CD7F28C3FFF3E7 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 632;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXXCSXXCG 17
Db 151 WSSWAQCSTSCG 162

RESULT 9
Q22580 Q22580 PRELIMINARY; PRT; 872 AA.
AC Q22580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T19D2.1;
GN Name=T19D2.1; ORFNames=T19D2.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid T19D2.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U42846; AAA83600.2; -.
DR PIR; T16892; T16892.
DR HSSP; P07996; 1LSL.
DR WormBase; WBGene00020567; T19D2.1.
DR WormPep; T19D2.1; CE30185.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP_1; 4.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50092; TSP1; 4.
```


DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 872 AA; 98040 MW; 1BA1D480AEF0ED15 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 872;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXXCSXXCG 17
Db 831 WSSWSSCSTKCG 842

RESULT 10
SM5A_MOUSE STANDARD; PRT; 1077 AA.
ID SM5A_MOUSE
AC Q62217;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 5A precursor (Semaphorin F) (Sema F).
GN Name=Sema5a; Synonyms=SemaF, SemF;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI;
RX MEDLINE=96414430; PubMed=8817451; DOI=10.1016/0925-4773(96)00525-4;
RA Adams R.H., Betz H., Pueschel A.W.;
RT "A novel class of murine semaphorins with homology to thrombospondin
is differentially expressed during early embryogenesis.";
RL Mech. Dev. 57:33-45(1996).
CC -!- FUNCTION: May act as positive axonal guidance cues.
CC -!- SUBUNIT: Binds PLXNB3 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In adult, detected in liver, brain, kidney,
heart, lung and spleen.
CC -!- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and
adult tissues. Its abundance decreases from E10 to birth.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 7 TSP type-1 domains.

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or send an email to license@isb-sib.ch).

DR EMBL; X97817; CAA66397.1; -.
DR HSSP; P07996; 1LSL.
DR MGD; MG1:107556; Sema5a.
DR GO; GO:0016021; C:integral to membrane; IDA.
DR GO; GO:0008046; F:axon guidance receptor activity; IDA.
DR GO; GO:0007411; P:axon guidance; IMP.
DR InterPro; IPR003659; plexin-like.
DR InterPro; IPR02165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR00884; TSP1.
DR InterPro; IPR008085; TSP1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP_1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 6.
DR PROSITE; PS51004; SEMA; 1.
DR PROSITE; PS50092; TSP1; 6.

KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
Repeat; Signal; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 1077 Semaphorin 5A.
FT DOMAIN 22 971 Extracellular (Potential).
FT TRANSMEM 972 992 Potential.
FT DOMAIN 993 1077 Cytoplasmic (Potential).
FT DOMAIN 35 484 Sema.
FT DOMAIN 540 593 TSP type-1 1.
FT DOMAIN 595 651 TSP type-1 2.
FT DOMAIN 653 702 TSP type-1 3.
FT DOMAIN 707 765 TSP type-1 4.
FT DOMAIN 784 839 TSP type-1 5.
FT DOMAIN 841 896 TSP type-1 6.
FT DOMAIN 897 944 TSP type-1 7.
FT DISULFID 104 114 By similarity.
FT DISULFID 131 140 By similarity.
FT DISULFID 278 320 By similarity.
FT DISULFID 487 504 By similarity.
FT DISULFID 496 513 By similarity.
FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 227 227 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 277 277 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 323 323 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 367 367 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 717 717 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 933 933 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1077 AA; 120826 MW; EDAB0DDDA42789FF CRC64;

Query Match 67.8%; Score 40; DB 1; Length 1077;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXXCSXXCG 17
Db 847 WSSWSKCSATCG 858

RESULT 11
Q6PCK8
ID Q6PCK8 PRELIMINARY; PRT; 1088 AA.
AC Q6PCK8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68835 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Fri Apr 1 15:03:07 2005

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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059288; AAH59288.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; P:development; IEA.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 5.
DR PROSITE; PS50092; TSP1; 6.
DR SEQUENCE 1088 AA; 122657 MW; 4DFCD371A7CD8176 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 1088;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
Db 608 WSSWAQCSTSCG 619

RESULT 12
Q6UY12 PRELIMINARY; PRT; 1092 AA.
AC Q6UY12;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SEMA5B.
GN ORFNames=UNQ5867;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.12933003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale

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RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358124; AAQ88491.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP 1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 5.
DR PROSITE; PS50092; TSP1; 5.
DR SEQUENCE 1092 AA; 119322 MW; 082BF746687C0AC5 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 1092;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
Db 670 WSSWALCSTSCG 681

RESULT 13
SMSB HUMAN
ID SMSB HUMAN STANDARD; PRT; 1093 AA.
AC Q9P283;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 5B precursor.
GN Name=SEMA5B; Synonyms=KIAA1445;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
CC -!- FUNCTION: May act as positive axonal guidance cues (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 7 TSP type-1 domains.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB040878; BAA95969.1; ALT_INIT.
CC Genew; HGNC:10737; SEMA5B.
CC InterPro; IPR003659; Plexin-like.
CC InterPro; IPR002165; Plexin_repeat.
CC InterPro; IPR001627; Sema.

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DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000885; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP 1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 5.
DR PROSITE; PS51004; Sema; 1.
DR PROSITE; PS50092; TSP1; 5.
KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 1093 Semaphorin 5B.
FT DOMAIN 20 978 Extracellular (Potential).
FT TRANSMEM 979 999 Potential.
FT DOMAIN 1000 1093 Cytoplasmic (Potential).
FT DOMAIN 45 495 Sema.
FT DOMAIN 551 605 TSP type-1 1.
FT DOMAIN 606 662 TSP type-1 2.
FT DOMAIN 664 713 TSP type-1 3.
FT DOMAIN 721 776 TSP type-1 4.
FT DOMAIN 795 850 TSP type-1 5.
FT DOMAIN 852 907 TSP type-1 6.
FT DOMAIN 908 952 TSP type-1 7.
FT CARBOHYD 59 59 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 287 287 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 333 333 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 378 378 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 532 532 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 539 539 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 547 547 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 602 602 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 728 728 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 944 944 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 1093 AA; 119866 MW; FIPDFB87CEAF0EF CRC64;

Query Match 67.8%; Score 40; DB 1; Length 1093;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCXXCG 17
Db 612 WSSWALCSTSCG 623

RESULT 14
SM5B_MOUSE
ID SM5B_MOUSE STANDARD; PRT; 1093 AA.
AC Q60519;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 5B precursor (Semaphorin G) (Sema G).
GN Name=Sema5b; Synonyms=SEMAG, SemG;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI;
RX MEDLINE=96414430; PubMed=8817451; DOI=10.1016/0925-4773(96)00525-4;
RA Adams R.H., Betz H., Püschel A.W.;
RT "A novel class of murine semaphorins with homology to thrombospondin
is differentially expressed during early embryogenesis.";
RL Mech. Dev. 57:33-45(1996).
CC -!- FUNCTION: May act as positive axonal guidance cues.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: In adult, only detected in brain.
CC -!- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and
CC adult tissues. Its abundance decreases from E10 to birth.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 7 TSP type-1 domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X97818; CAA66398.1; -.
CC HSSP; P07996; 1LSL.
CC MGD; MGI:107555; Sema5b.
CC InterPro; IPR003659; Plexin-like.
CC InterPro; IPR002165; Plexin_repeat.
CC InterPro; IPR001627; Sema.
CC InterPro; IPR000884; TSP1.
CC InterPro; IPR008085; TSP_1.
CC Pfam; PF01437; PSI; 1.
CC Pfam; PF01403; Sema; 1.
CC Pfam; PF00090; TSP 1; 5.
CC PRINTS; PR01705; TSP1REPEAT.
CC SMART; SM00423; PSI; 1.
CC SMART; SM00630; Sema; 1.
CC SMART; SM00209; TSP1; 5.
CC PROSITE; PS51004; Sema; 1.
CC PROSITE; PS50092; TSP1; 5.
KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1093 Semaphorin 5B.
FT DOMAIN 20 978 Extracellular (Potential).
FT TRANSMEM 979 999 Potential.
FT DOMAIN 1000 1093 Cytoplasmic (Potential).
FT DOMAIN 45 495 Sema.
FT DOMAIN 551 605 TSP type-1 1.
FT DOMAIN 606 662 TSP type-1 2.
FT DOMAIN 664 713 TSP type-1 3.
FT DOMAIN 721 776 TSP type-1 4.
FT DOMAIN 795 850 TSP type-1 5.
FT DOMAIN 852 907 TSP type-1 6.
FT DOMAIN 908 952 TSP type-1 7.
FT CARBOHYD 59 59 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 95 95 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 287 287 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 333 333 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 378 378 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 532 532 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 539 539 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 547 547 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 602 602 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 728 728 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 944 944 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 1093 AA; 120326 MW; 29E5C9B1E8108717 CRC64;

Query Match 67.8%; Score 40; DB 1; Length 1093;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCXXCG 17
Db 612 WSSWALCSTSCG 623

RESULT 15
Q7QC32

ID Q7QC32 PRELIMINARY; PRT; 1093 AA.
AC Q7QC32;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Ebip1179 (Fragment).
GN Name=ebiG1179; ORFNames=ENSANGG00000001015;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008859; EAA07529.1; -.
DR HSSP; Q92854; IOLZ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP_1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR PROSITE; PS50092; TSP1; 5.
FT NON_TER 1
FT NON_TER 1093
FT NON_TER 1093
SQ SEQUENCE 1093 AA; 118842 MW; 2DB86BEC7CB42230 CRC64;

Query Match 67.8%; Score 40; DB 2; Length 1093;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXCSXXCG 17
Db 586 WSAWSACSTCG 597

Search completed: April 1, 2005, 13:59:24
Job time : 139.696 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:43:07 ; Search time 30.6087 Seconds
(without alignments)
69.156 Million cell updates/sec

Title: US-09-462-909D-9
Perfect score: 59
Sequence: 1 XXXXXWSXXXCSXXCGXXXXX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	67.8	860	Ti6892	hypothetical prote
2	40	67.8	1170	1 TSHUP1	thrombospondin 1 p
3	40	67.8	1170	2 A40558	thrombospondin 1 p
4	39	66.1	206	2 A45517	coccidioidis-relate
5	39	66.1	610	2 T16761	hypothetical prote
6	39	66.1	654	2 T29247	hypothetical prote
7	39	66.1	712	2 A45638	immunodominant mic
8	39	66.1	724	2 A48569	antigen Em100 - Ei
9	39	66.1	984	2 T00326	hypothetical prote
10	39	66.1	1444	2 T18856	angiogenesis inhib
11	39	66.1	1522	2 T00028	brain-specific ang
12	39	66.1	2098	2 T18397	protein CTRP - mal
13	38	64.4	788	2 T25061	hypothetical prote
14	38	64.4	803	2 A47723	F-spondin precursor
15	38	64.4	807	2 A38152	F-spondin - rat
16	38	64.4	957	2 T15976	hypothetical prote
17	38	64.4	1074	2 JC5928	semaphorin F precu
18	38	64.4	1172	1 TSHUP2	thrombospondin 2 p
19	38	64.4	1172	2 A42587	thrombospondin 2 p
20	38	64.4	1178	1 A39804	thrombospondin pre
21	38	64.4	1184	2 T09484	cartilage intermed
22	38	64.4	1205	2 T18517	procollagen N-endo
23	38	64.4	1584	2 T00026	brain-specific ang
24	37	62.7	437	2 S05478	properdin - mouse
25	37	62.7	551	2 T16557	hypothetical prote
26	37	62.7	805	2 T34212	hypothetical prote
27	37	62.7	1360	2 T33922	hypothetical prote
28	37	62.7	1572	2 T00027	brain-specific ang
29	35	59.3	1059	2 T22545	hypothetical prote

30	34	57.6	49	2	H53613	plectoxin X - spid
31	34	57.6	123	2	S49108	TRAP-C2 protein -
32	34	57.6	293	2	T20523	hypothetical prote
33	34	57.6	334	2	T20524	hypothetical prote
34	34	57.6	651	2	T19477	hypothetical prote
35	34	57.6	919	2	T32541	unc-5 protein - Ca
36	34	57.6	947	1	B44294	unc-5 protein, lon
37	33	55.9	291	2	T28846	hypothetical prote
38	33	55.9	559	2	S04531	thrombospondin-rel
39	33	55.9	574	2	A46283	sporozoite surface
40	33	55.9	703	2	T04191	hypothetical prote
41	33	55.9	736	2	T19366	hypothetical prote
42	33	55.9	2165	2	T21371	hypothetical prote
43	32	54.2	469	1	S29126	properdin precursor
44	32	54.2	550	2	T47158	hypothetical prote
45	32	54.2	837	2	T00355	hypothetical prote

ALIGNMENTS

RESULT 1

T16892
hypothetical protein T19D2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16892
R;Bentley, D.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19D2.
A;Reference number: Z18599
A;Accession: T16892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-860 <BEN>
A;Cross-references: UNIPROT:Q22580; EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA8360
C;Genetics:
A;Gene: CESP:T19D2.1
A;Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 582/3

Query Match 67.8%; Score 40; DB 2; Length 860;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	6	WSXXXCSXXCG 17
Db	831	WSSWSCSTKCG 842

RESULT 2

TSHUP1
thrombospondin 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1987 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A26155; A34274; A30140; A25812; A05172; A42927
R;Lawler, J.; Hynes, R.O.
J. Cell Biol. 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple ca
A;Reference number: A26155; MUID:87057617; PMID:2430973
A;Accession: A26155
A;Molecule type: mRNA
A;Residues: 1-1170 <LAH>
A;Cross-references: UNIPROT:P07996; GB:X04665; NID:g37137; PIDN:CAA28370.1; PID:g37138
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
R;Lahterty, C.D.; Gierman, T.M.; Dixit, V.M.
J. Biol. Chem. 264, 11222-11227, 1989
A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA se
A;Reference number: A34274; MUID:89291870; PMID:2544587
A;Accession: A34274
A;Molecule type: DNA
A;Residues: 1-166 <LAH>
A;Cross-references: GB:J04835
R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein, F

J. Cell Biol. 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in the 5' and 3' noncoding regions
A;Reference number: A30140; MUID:89139590; PMID:2918029
A;Accession: A30140
A;Molecule type: mRNA
A;Residues: 1-83, 'A', 85-522, 'A', 524-1170 <HEN>
A;Cross-references: EMBL:X14787; NID:G37464; PIDN:CAA32889.1; PID:G37465
A;Note: parts of this sequence, including the amino end of the mature protein, were determined by analysis of cDNA clones
R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones
A;Reference number: A25812; MUID:87157592; PMID:3030396
A;Accession: A25812
A;Molecule type: mRNA
A;Residues: 1-83, 'A', 85-397 <KOB>
A;Cross-references: GB:M25631; NID:G538353; PIDN:AAA36741.1; PID:G538354
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A;Reference number: A05172; MUID:86287276; PMID:3461443
A;Accession: A05172
A;Molecule type: mRNA
A;Residues: 1-83, 'A', 85-374, 'RC' <DIX>
A;Cross-references: GB:M14326; NID:G340005; PIDN:AAA61237.1; PID:G553801
A;Note: parts of this sequence, including the amino end of the mature protein, were determined by analysis of cDNA clones
R;Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A;Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A;Reference number: A42927; MUID:92348511; PMID:1379247
A;Accession: A42927
A;Molecule type: protein
A;Residues: 987-1003 <SUN>
A;Note: Cys-992 is shown to have a free sulfhydryl
C;Genetics:
A;Gene: GDB:THBS1; TSP1; TSP
A;Cross-references: GDB:120438; OMIM:188060
A;Map position: 15q15-15q15
A;Introns: 23/1
A;Note: the list of introns may be incomplete
C;Complex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology; calcium binding; cell adhesion; glycoprotein; trimer
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF1>
F;650-689/Domain: EGF homology <EGF2>
F;926-928/Region: cell attachment (R-G-D) motif
F;171-232/Disulfide bonds: #status predicted
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;270,274/Disulfide bonds: interchain #status predicted
F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status absent
F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 67.8%; Score 40; DB 1; Length 1170;
Best Local Similarity 50.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 6 WSXXXXCSXXCG 17
DB 385 WSEWTSCTSCG 396

RESULT 3
A40558
thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787

R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
Genomics 11, 587-600, 1991
A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
A;Accession: A40558
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1170 <LAW>
A;Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453;
; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:951181
R;Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A;Title: Characterization of the mouse thrombospondin gene and evaluation of the role of the 5' noncoding region
A;Reference number: A37905; MUID:90375546; PMID:2398070
A;Accession: A37905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <BOR>
A;Cross-references: GB:J05605; GB:J05606; NID:G201991; PIDN:AAA40431.1; PID:G554390
R;Laberty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell differentiation
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: B42587
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1152, 'P', 1154-1170 <LAH>
A;Cross-references: GB:M87276
A;Note: sequence extracted from NCBI backbone (NCBIP:81501)
R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 and 2
A;Reference number: S68787; MUID:96234006; PMID:8654563
A;Accession: S68787
A;Molecule type: protein
A;Residues: 19-26, 'X', 28-37 <CHE>
C;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von Willebrand factor type C repeat homology; glycoprotein; homotrimer
C;Keywords: calcium binding; glycoprotein; signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <MAT>
F;19-1170/Product: thrombospondin 1 #status predicted <VWC>
F;317-375/Domain: von Willebrand factor type C repeat homology <THR1>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR2>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR3>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF>
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.8%; Score 40; DB 2; Length 1170;
Best Local Similarity 50.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 6 WSXXXXCSXXCG 17
DB 385 WSEWTSCTSCG 396

RESULT 4
A45517
coccidioides-related antigen - Eimeria tenella (fragment)
N;Alternate names: thrombospondin-related antigen, 100K
C;Species: Eimeria tenella
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C;Accession: A45517; S27818
R;Clarke, L.E.; Tomley, F.M.; Wisner, M.H.; Foulds, I.J.; Boursnell, M.E.G.
Mol. Biochem. Parasitol. 41, 269-280, 1990
A;Title: Regions of an Eimeria tenella antigen contain sequences which are conserved in other eimeria antigens
A;Reference number: A45517; MUID:90377296; PMID:2204833
A;Accession: A45517
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <CLA>
A;Cross-references: UNIPROT:Q24927; GB:M32988; NID:G158870; PID:G158871

F;136-198/Domain: thrombospondin type 1 repeat homology <THR5>

Query Match 66.1%; Score 39; DB 2; Length 206;
Best Local Similarity 50.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
|| || || ||
Db 21 WSEWTECSATCG 32

RESULT 5

T16761

hypothetical protein R151.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Dec-2002

C;Accession: T16761

R;Fulton, L.

submitted to the EMBL Data Library, February 1994

A;Description: The sequence of C. elegans cosmid R151.

A;Reference number: S44639

A;Accession: T16761

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-610 <FUL>

A;Cross-references: EMBL:U00036; NID:g458996; PID:g459001; PIDN:AAA50653.1; CESP:R151.5

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:R151.5

A;Introns: 68/3; 120/1; 151/1; 307/1; 448/2; 525/2; 567/2; 592/2

C;Superfamily: metalloproteinase hch-1; astacin homology

Query Match

Best Local Similarity 66.1%; Score 39; DB 2; Length 610;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17

|| || || ||

Db 496 WSPWTACSATCG 507

RESULT 6

T29247

hypothetical protein F09F9.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T29247

R;Minx, P.; Hawkins, J.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid F09F9.

A;Reference number: Z20594

A;Accession: T29247

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-654 <MIN>

A;Cross-references: UNIPROT:Q19284; EMBL:U40958; PIDN:AAA81764.1; CESP:F09F9.4

C;Genetics:

A;Gene: CESP:F09F9.4

A;Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

Query Match

Best Local Similarity 66.1%; Score 39; DB 2; Length 654;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17

|| || || ||

Db 322 WSEWSACSETCG 333

RESULT 7

A45638

immunodominant microneme protein Etp100 - Eimeria tenella

C;Species: Eimeria tenella

C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A45638

R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.

Mol. Biochem. Parasitol. 49, 277-288, 1991

A;Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria tenella

A;Reference number: A45638; MUID:92131064; PMID:1775171

A;Accession: A45638

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-712 <TOM>

A;Cross-references: UNIPROT:O43981; GB:AF032905; GB:M73495; NID:g2707732; PIDN:AAD03350.1

A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)

F;48-218/Domain: von Willebrand factor type A repeat homology <VWA1>

F;238-296/Domain: thrombospondin type 1 repeat homology <THR1>

F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>

F;372-432/Domain: thrombospondin type 1 repeat homology <THR3>

F;433-493/Domain: thrombospondin type 1 repeat homology <THR4>

F;494-556/Domain: thrombospondin type 1 repeat homology <THR5>

F;560-610/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 66.1%; Score 39; DB 2; Length 712;

Best Local Similarity 50.0%; Pred. No. 5.6;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17

|| || || ||

Db 379 WSEWTECSATCG 390

RESULT 8

A48569

antigen Eml00 - Eimeria maxima

C;Species: Eimeria maxima

C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A48569

R;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.

Mol. Biochem. Parasitol. 57, 171-174, 1993

A;Title: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella mic

A;Reference number: A48569; MUID:93149203; PMID:8426611

A;Accession: A48569

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-724 <PAS>

A;Cross-references: UNIPROT:Q04588; GB:M99058; NID:g158890; PID:g158891

A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)

F;45-218/Domain: von Willebrand factor type A repeat homology <VWA2>

F;238-296/Domain: thrombospondin type 1 repeat homology <THR1>

F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>

F;372-432/Domain: thrombospondin type 1 repeat homology <THR3>

F;433-493/Domain: thrombospondin type 1 repeat homology <THR4>

F;494-556/Domain: thrombospondin type 1 repeat homology <THR5>

F;560-610/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match

Best Local Similarity 66.1%; Score 39; DB 2; Length 724;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17

|| || || ||

Db 379 WSDWSDCSATCG 390

RESULT 9

T00326

hypothetical protein KIAA0550 - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 15-Mar-2004

C;Accession: T00326

R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.

DNA Res. 5, 31-39, 1998

A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete

A;Reference number: Z14086; MUID:98290545; PMID:9628581

A;Accession: T00326

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-984 <NAG>
A;Cross-references: EMBL:AB011122; NID:G3043623; PIDN:BAA25476.1; PID:G3043624
A;Experimental source: brain
C;Genetics:
A;Note: KIAA0550
F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 66.1%; Score 39; DB 2; Length 984;
Best Local Similarity 50.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXXCG 17
|| || ||
Db 297 WSQWSTCSTCTCG 308

RESULT 10
T18856
angiogenesis inhibitor homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18856; T24653
R;McMurray, A.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19031
A;Accession: T18856
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1444 <WT>
A;Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4.1
A;Experimental source: clone C02B4
R;McMurray, A.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19917
A;Accession: T24653
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1444 <WT2>
A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1
A;Experimental source: clone T07C5
C;Genetics:
A;Gene: CESP:C02B4.1
A;Map position: X
A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/3

Query Match 66.1%; Score 39; DB 2; Length 1444;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXXCG 17
|| || ||
Db 696 WSSWSECSVSCG 707

RESULT 11
T00028
brain-specific angiogenesis inhibitor 3 - human
N;Alternate names: BAI3 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00028
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-
A;Reference number: Z14066; MUID:98194217; PMID:9533023
A;Accession: T00028
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1522 <SHI>
A;Cross-references: UNIPROT:O60242; EMBL:AB005299; NID:G3021700; PIDN:BAA25363.1; PID:G3021700
A;Experimental source: brain

C;Genetics:
A;Gene: GDB:BAI3
A;Cross-references: GDB:9838090; OMIM:602684
A;Map position: 6q12-6q12
F;344-398/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 66.1%; Score 39; DB 2; Length 1522;
Best Local Similarity 50.0%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXXCG 17
|| || ||
Db 297 WSQWSTCSTCTCG 308

RESULT 12
T18397
protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397
R;Trottein, F.; Triglia, T.; Cowman, A.F.
Mol. Biochem. Parasitol. 74, 129-142, 1995
A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein
A;Reference number: Z18926; MUID:96360471; PMID:8719155
A;Accession: T18397
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2098 <TRO>
A;Cross-references: UNIPROT:Q25757; EMBL:U34363; NID:G1098897; PID:G1098898; PIDN:AAC4694

Query Match 66.1%; Score 39; DB 2; Length 2098;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXXCG 17
|| || ||
Db 1644 WSDWSSCSKTCTCG 1655

RESULT 13
T25061
hypothetical protein T21B6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25061
R;Cottage, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19975
A;Accession: T25061
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-788 <WIL>
A;Cross-references: UNIPROT:Q22631; EMBL:Z68011; PIDN:CAA92014.1; GSPDB:GN00028; CESP:T2
A;Experimental source: clone T21B6
C;Genetics:
A;Gene: CESP:T21B6.3
A;Map position: X
A;Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2

Query Match 64.4%; Score 38; DB 2; Length 788;
Best Local Similarity 50.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXXCG 17
|| || ||
Db 461 WSDWSTCSTCTCG 472

RESULT 14
A47723
F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)

C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47723
R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A;Reference number: A47723; MUID:93376785; PMID:8367492
A;Accession: A47723
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-803 <RUI>
A;Cross-references: UNIPROT:P35447; GB:L09123; NID:g409244; PIDN:AAA19105.1; PID:g409245
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 64.4%; Score 38; DB 2; Length 803;
Best Local Similarity 50.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXCSXXCG 17
Db 614 WSEWSDCSVTCG 625

RESULT 15
A38152
F-spondin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A38152
R;Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secreted
A;Reference number: A38152; MUID:92208952; PMID:1555244
A;Accession: A38152
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-807 <KLA>
A;Cross-references: UNIPROT:P35446; GB:M88469; NID:g204176; PIDN:AAA41174.1; PID:g204177
A;Experimental source: embryo floor plate
A;Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;441-495/Domain: thrombospondin type 1 repeat homology <THR2>
F;500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F;557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F;613-666/Domain: thrombospondin type 1 repeat homology <THR1>
F;667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F;753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 64.4%; Score 38; DB 2; Length 807;
Best Local Similarity 50.0%; Pred. No. 9.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 WSXXXCSXXCG 17
Db 620 WSEWSDCSVTCG 631

Search completed: April 1, 2005, 14:00:31
Job time : 31.6087 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:59:39 ; Search time 113.348 Seconds
(without alignments)
64.360 Million cell updates/sec

Title: US-09-462-909D-9
Perfect score: 59
Sequence: 1 XXXXXWSXXXCSXXCGXXXXX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	40	67.8	23	14	US-10-042-696-11
2	40	67.8	50	10	US-09-373-658-6
3	40	67.8	50	11	US-09-989-687-6
4	40	67.8	50	15	US-10-019-065A-6
5	40	67.8	51	17	US-10-883-144-35
6	40	67.8	143	15	US-10-276-774-1454
7	40	67.8	170	15	US-10-419-462-43
8	40	67.8	170	16	US-10-296-733-20
9	40	67.8	170	17	US-10-782-968-43
10	40	67.8	218	13	US-10-036-869-1
11	40	67.8	397	17	US-10-454-246-20
12	40	67.8	401	15	US-10-190-115-111
13	40	67.8	401	15	US-10-190-115-114

14	40	67.8	401	15	US-10-190-115-116	Sequence 116, Appl
15	40	67.8	401	15	US-10-190-115-118	Sequence 118, Appl
16	40	67.8	401	17	US-10-454-246-10	Sequence 10, Appl
17	40	67.8	401	17	US-10-454-246-12	Sequence 12, Appl
18	40	67.8	401	17	US-10-454-246-14	Sequence 14, Appl
19	40	67.8	401	17	US-10-454-246-16	Sequence 16, Appl
20	40	67.8	432	17	US-10-741-600-1020	Sequence 1020, Ap
21	40	67.8	432	17	US-10-741-600-1022	Sequence 1022, Ap
22	40	67.8	441	13	US-10-036-869-3	Sequence 3, Appli
23	40	67.8	466	9	US-09-925-301-1047	Sequence 1047, Ap
24	40	67.8	606	14	US-10-234-432-70	Sequence 70, Appl
25	40	67.8	831	11	US-09-939-853A-97	Sequence 97, Appl
26	40	67.8	831	11	US-09-939-853A-98	Sequence 98, Appl
27	40	67.8	939	9	US-09-854-845-16	Sequence 16, Appl
28	40	67.8	939	17	US-10-833-509-16	Sequence 16, Appl
29	40	67.8	954	9	US-09-854-845-14	Sequence 14, Appl
30	40	67.8	954	17	US-10-833-509-14	Sequence 14, Appl
31	40	67.8	1034	9	US-09-854-845-6	Sequence 6, Appli
32	40	67.8	1034	17	US-10-833-509-6	Sequence 6, Appli
33	40	67.8	1049	9	US-09-854-845-2	Sequence 2, Appli
34	40	67.8	1049	17	US-10-833-509-2	Sequence 2, Appli
35	40	67.8	1077	15	US-10-190-115-43	Sequence 43, Appl
36	40	67.8	1077	15	US-10-369-072-43	Sequence 43, Appl
37	40	67.8	1078	9	US-09-854-845-8	Sequence 8, Appli
38	40	67.8	1078	17	US-10-833-509-8	Sequence 8, Appli
39	40	67.8	1092	14	US-10-245-752-96	Sequence 96, Appl
40	40	67.8	1092	14	US-10-245-859-96	Sequence 96, Appl
41	40	67.8	1092	14	US-10-245-103-96	Sequence 96, Appl
42	40	67.8	1092	14	US-10-245-107-96	Sequence 96, Appl
43	40	67.8	1092	14	US-10-245-143-96	Sequence 96, Appl
44	40	67.8	1092	14	US-10-245-771-96	Sequence 96, Appl
45	40	67.8	1092	14	US-10-245-851-96	Sequence 96, Appl

ALIGNMENTS

RESULT 1

US-10-042-696-11
; Sequence 11, Application US/10042696
; Publication No. US20030171298A1
; GENERAL INFORMATION:
; APPLICANT: Tuszynski, George
; APPLICANT: Williams, Taffy
; APPLICANT: Actor, Paul
; TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT THROMBOSPONDIN ACT
; FILE REFERENCE: 07206-0021
; CURRENT APPLICATION NUMBER: US/10/042,696
; CURRENT FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic fragment/analog of
; OTHER INFORMATION: thrombospondin
US-10-042-696-11

Query Match 67.8%; Score 40; DB 14; Length 23;
Best Local Similarity 50.0%; Pred. No. 6.7;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17

Db 4 WSEWTSCTSCG 15

RESULT 2

US-09-373-658-6
; Sequence 6, Application US/09373658
; Publication No. US20030092900A1

Fri Apr 1 15:03:06 2005

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; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-373-658-6

Query Match      67.8%; Score 40; DB 10; Length 50;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WXXXXXCSXXCG 17
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Db      7 WSEWTSCTSCG 18

RESULT 3
US-09-989-687-6
; Sequence 6, Application US/099899687
; Publication No. US20040002449A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.107000D
; CURRENT APPLICATION NUMBER: US/09/989,687
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-687-6

Query Match      67.8%; Score 40; DB 11; Length 50;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WXXXXXCSXXCG 17
      |||||
Db      7 WSEWTSCTSCG 18

RESULT 4
US-10-019-065A-6
; Sequence 6, Application US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCT
; CURRENT APPLICATION NUMBER: US/10/019,065A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 50
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated type 1 thrombospondin domain sequence
US-10-019-065A-6

Query Match      67.8%; Score 40; DB 15; Length 50;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WXXXXXCSXXCG 17
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Db      6 WSEWTSCTSCG 17

RESULT 5
US-10-883-144-35
; Sequence 35, Application US/10883144
; Publication No. US20050054829A1
; GENERAL INFORMATION:
; APPLICANT: IMMUNEX CORPORATION
; APPLICANT: Wiley, Steven R.
; APPLICANT: Vakili, Jalaleddin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO TSP-30a, b, c AND d
; FILE REFERENCE: 3474-A
; CURRENT APPLICATION NUMBER: US/10/883,144
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 60/489,409
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-883-144-35

Query Match      67.8%; Score 40; DB 17; Length 51;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WXXXXXCSXXCG 17
      |||||
Db      7 WSEWTSCTSCG 18

RESULT 6
US-10-276-774-1454
; Sequence 1454, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1454
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1454

Query Match      67.8%; Score 40; DB 15; Length 143;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 6 WSXXXXCSXXCG 17
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Db 89 WSSWALCSTSCG 100

RESULT 7

US-10-419-462-43

; Sequence 43, Application US/10419462

; Publication No. US20040053392A1

; GENERAL INFORMATION:

; APPLICANT: Kevin J. Williams

; APPLICANT: Williams, Kevin J.

; TITLE OF INVENTION: Thrombospondin Fragments and Uses Thereof In Clinical Assays for

; FILE REFERENCE: W1107-20005 Cancer and Generation of Antibodies and Other Binding Agents

; CURRENT APPLICATION NUMBER: US/10/419,462

; CURRENT FILING DATE: 2003-04-17

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 43

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Thrombospondin Region plus Domain of type 1 repeats

US-10-419-462-43

Query Match

Best Local Similarity 67.8%; Score 40; DB 15; Length 170;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17

|||

Db 7 WSEWTSCSTSCG 18

RESULT 8

US-10-296-733-20

; Sequence 20, Application US/10296733

; Publication No. US20040110131A1

; GENERAL INFORMATION:

; APPLICANT: Beth Israel Deaconess Medical Center

; APPLICANT: Lawler, John W.

; TITLE OF INVENTION: Thrombospondin-1 Type 1 Repeat

; FILE REFERENCE: 1440.2009002 Polypeptides

; CURRENT APPLICATION NUMBER: US/10/296,733

; CURRENT FILING DATE: 2002-11-25

; PRIOR APPLICATION NUMBER: 60/207,994

; PRIOR FILING DATE: 2000-05-26

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-296-733-20

Query Match

Best Local Similarity 67.8%; Score 40; DB 16; Length 170;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17

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Db 7 WSEWTSCSTSCG 18

RESULT 9

US-10-782-968-43

; Sequence 43, Application US/10782968

; Publication No. US20050065324A1

; GENERAL INFORMATION:

; APPLICANT: Kevin J. Williams

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Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WSXXXCSXXCG 17
Db 85 WSEWTSCTSCG 96

RESULT 11
US-10-454-246-20
; Sequence 20, Application US/10454246
; Publication No. US20050053930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 B
; CURRENT APPLICATION NUMBER: US/10/454,246
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/218,903
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 10/016,248
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 10/136,071
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/289,087
; PRIOR FILING DATE: 2001-05-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 339
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 20
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Domain
US-10-454-246-20

Query Match 67.8%; Score 40; DB 17; Length 397;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
Db 58 WSSWALCSTSCG 69

RESULT 12
US-10-190-115-111
; Sequence 111, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
```

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; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 111
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-190-115-111

Query Match 67.8%; Score 40; DB 15; Length 401;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
Db 60 WSSWALCSTSCG 71

RESULT 13
US-10-190-115-114
; Sequence 114, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
```

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; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 114
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-114.

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Query Match      67.8%; Score 40; DB 15; Length 401;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY      6 WSXXXXCSXXCG 17
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Db      60 WSSWALCSTSCG 71

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RESULT 14
US-10-190-115-116
; Sequence 116, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.

```

```

; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 116
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-116

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Query Match      67.8%; Score 40; DB 15; Length 401;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY      6 WSXXXXCSXXCG 17
      |||||
Db      60 WSSWALCSTSCG 71

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RESULT 15
US-10-190-115-118
; Sequence 118, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.

```

APPLICANT: Tchernev, Velizar T.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Voss, Edward Z.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-050 CIP
CURRENT APPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/368,996
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/386,816
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,585,
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 118
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
US-10-190-115-118

Query Match 67.8%; Score 40; DB 15; Length 401;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 WXXXXXCSXXCG 17
Db 60 WSSWALCSTSCG 71

Search completed: April 1, 2005, 14:22:18
Job time : 114.348 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:44:22 ; Search time 38.7391 Seconds
(without alignments)
42.393 Million cell updates/sec

Title: US-09-462-909D-9
Perfect score: 59
Sequence: 1 XXXXXWSXXXXCSXXCGXXXXX 22

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	67.8	23	1	US-07-646-531D-5
2	40	67.8	23	2	US-08-488-273-5
3	40	67.8	23	3	US-09-197-770B-11
4	40	67.8	23	6	5426100-5
5	40	67.8	23	6	5426100-5
6	40	67.8	218	3	US-08-985-526-1
7	40	67.8	239	5	PCT-US93-01652-1
8	40	67.8	441	3	US-08-985-526-3
9	40	67.8	939	4	US-09-854-845-16
10	40	67.8	954	4	US-09-854-845-14
11	40	67.8	1034	4	US-09-854-845-6
12	40	67.8	1049	4	US-09-854-845-2
13	40	67.8	1078	4	US-09-854-845-8
14	40	67.8	1093	4	US-09-854-845-4
15	40	67.8	1136	4	US-09-854-845-12
16	40	67.8	1151	4	US-09-854-845-10
17	40	67.8	1170	1	US-08-313-288B-20
18	40	67.8	1170	4	US-09-657-472-2
19	39	66.1	120	4	US-09-270-767-32422
20	39	66.1	120	4	US-09-270-767-47639
21	39	66.1	479	4	US-09-270-767-46823
22	39	66.1	677	4	US-09-270-767-58094
23	39	66.1	847	4	US-09-270-767-42783
24	39	66.1	874	3	US-09-369-364A-15
25	39	66.1	997	3	US-09-369-364A-7
26	38	64.4	23	1	US-07-646-531D-6
27	38	64.4	23	2	US-08-488-273-6

28	38	64.4	23	3	US-09-197-770B-12	Sequence 12, Appl
29	38	64.4	23	6	5426100-6	Patent No. 5426100
30	38	64.4	23	6	5426100-6	Patent No. 5426100
31	38	64.4	51	2	US-08-799-173A-11	Sequence 11, Appl
32	38	64.4	51	4	US-09-170-042A-11	Sequence 11, Appl
33	38	64.4	60	1	US-07-646-531D-12	Sequence 12, Appl
34	38	64.4	60	2	US-08-488-273-12	Sequence 12, Appl
35	38	64.4	60	6	5426100-12	Patent No. 5426100
36	38	64.4	60	6	5426100-12	Patent No. 5426100
37	38	64.4	568	1	US-07-862-021B-14	Sequence 14, Appl
38	38	64.4	568	5	PCT-US93-03164-14	Sequence 14, Appl
39	38	64.4	787	4	US-09-825-294-207	Sequence 207, App
40	38	64.4	787	4	US-09-970-966-207	Sequence 207, App
41	38	64.4	788	2	US-08-918-914-4	Sequence 4, Appl
42	38	64.4	802	1	US-07-862-021B-12	Sequence 12, Appl
43	38	64.4	802	1	US-08-313-288B-12	Sequence 12, Appl
44	38	64.4	802	5	PCT-US93-03164-12	Sequence 12, Appl
45	38	64.4	807	1	US-07-862-021B-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-07-646-531D-5
; Sequence 5, Application US/07646531D
; Patent No. 5200397
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan Howard
; APPLICANT: Tuszyński, George Paul
; TITLE OF INVENTION: Peptide Fragments and Analogs of
; TITLE OF INVENTION: Thrombospondin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. R. Grace & Co.-Conn.
; STREET: 7379 Route 32
; CITY: Columbia
; STATE: Maryland
; COUNTRY: USA
; ZIP: 21044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,531D
; FILING DATE: 19910131
; ATTORNEY/AGENT INFORMATION:
; NAME: Appleby, Vanessa L.
; REGISTRATION NUMBER: 33223
; REFERENCE/DOCKET NUMBER: 01-7896
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 531-4515
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-646-531D-5

Query Match 67.8%; Score 40; DB 1; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSXXCG 17
|||
Db 4 WSEWTSCTSCG 15

RESULT 2
US-08-488-273-5

Fri Apr 1 15:03:06 2005

; Sequence 5, Application US/08488273
; Patent No. 5840692
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan H.
; APPLICANT: Tuszyński, George P.
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; TITLE OF INVENTION: THROMBOSPONDIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,273
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/359,263
; FILING DATE: 19-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,527
; FILING DATE: 09-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/483,527
; FILING DATE: 22-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-2U4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-273-5

Query Match 67.8%; Score 40; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
||| |||
Db 4 WSEWTSCTSCG 15

RESULT 3
US-09-197-770B-11
; Sequence 11, Application US/09197770B
; Patent No. 6339062
; GENERAL INFORMATION:
; APPLICANT: Tuszyński, George
; APPLICANT: Williams, Taffy
; APPLICANT: Actor, Paul
; TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
; TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
; FILE REFERENCE: 07206-0021

; CURRENT APPLICATION NUMBER: US/09/197,770B
; CURRENT FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770B-11

Query Match 67.8%; Score 40; DB 3; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
||| |||
Db 4 WSEWTSCTSCG 15

RESULT 4
5426100-5
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO: 5:
; LENGTH: 23
5426100-5

Query Match 67.8%; Score 40; DB 6; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
||| |||
Db 4 WSEWTSCTSCG 15

RESULT 5
5426100-5
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO: 5:
; LENGTH: 23
5426100-5

Query Match 67.8%; Score 40; DB 6; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
|| || ||
Db 4 WSEWTSCTSCG 15

RESULT 6

US-08-985-526-1
; Sequence 1, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-1

Query Match 67.8%; Score 40; DB 3; Length 218;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
|| || ||
Db 85 WSEWTSCTSCG 96

RESULT 7

PCT-US93-01652-1
; Sequence 1, Application PC/TUS9301652
; GENERAL INFORMATION:
; APPLICANT: Bouck, Noel P.
; APPLICANT: Polverini, Peter J.
; APPLICANT: Good, Deborah J.
; APPLICANT: Frazier, William A.
; TITLE OF INVENTION: Method and Composition for
; TITLE OF INVENTION: Inhibiting Angiogenesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01652
; FILING DATE: 19930222
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,656
; FILING DATE: 24-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/464,369
; FILING DATE: 12-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fentress, Susan B.
; REGISTRATION NUMBER: 31,327
; REFERENCE/DOCKET NUMBER: 92005-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)-456-8000
; TELEFAX: (312)-456-7776
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US93-01652-1

Query Match 67.8%; Score 40; DB 5; Length 239;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
|| || || ||
Db 74 WSEWTSCTSCG 85

RESULT 8

US-08-985-526-3
; Sequence 3, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141

```

; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-985-526-3

Query Match          67.8%; Score 40; DB 3; Length 441;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WSXXXCSXXCG 17
Db      85 WSEWTSCSTSCG 96

RESULT 9
US-09-854-845-16
; Sequence 16, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 939
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-16

Query Match          67.8%; Score 40; DB 4; Length 939;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WSXXXCSXXCG 17
Db      473 WSSWALCSTSCG 484

RESULT 10
US-09-854-845-14
; Sequence 14, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 954
; TYPE: PRT

```

```

; ORGANISM: homo sapiens
US-09-854-845-14

Query Match          67.8%; Score 40; DB 4; Length 954;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WSXXXCSXXCG 17
Db      473 WSSWALCSTSCG 484

RESULT 11
US-09-854-845-6
; Sequence 6, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-6

Query Match          67.8%; Score 40; DB 4; Length 1034;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 WSXXXCSXXCG 17
Db      568 WSSWALCSTSCG 579

RESULT 12
US-09-854-845-2
; Sequence 2, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-2

Query Match          67.8%; Score 40; DB 4; Length 1049;
Best Local Similarity 50.0%; Pred. No. 94;

```

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
Db 568 WSSWALCSTSCG 579

RESULT 13
US-09-854-845-8
; Sequence 8, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-8

Query Match 67.8%; Score 40; DB 4; Length 1078;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
Db 612 WSSWALCSTSCG 623

RESULT 14
US-09-854-845-4
; Sequence 4, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1093
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-4

Query Match 67.8%; Score 40; DB 4; Length 1093;
Best Local Similarity 50.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
Db 612 WSSWALCSTSCG 623

RESULT 15
US-09-854-845-12
; Sequence 12, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1136
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-12

Query Match 67.8%; Score 40; DB 4; Length 1136;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
Db 670 WSSWALCSTSCG 681

Search completed: April 1, 2005, 14:01:58
Job time : 39.7391 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:22:55 ; Search time 153.522 Seconds
(without alignments)
55.424 Million cell updates/sec

Title: US-09-462-909D-9
Perfect score: 59
Sequence: 1 XXXXXWSXXXCSXXCGXXXXX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	67.8	23	AAR13629	Aar13629 Thrombosp
2	40	67.8	23	AAW81482	Aaw81482 Thrombosp
3	40	67.8	23	AAE20746	Aae20746 Thrombosp
4	40	67.8	23	ADM80537	Adm80537 Thrombosp
5	40	67.8	50	AAY49503	Aay49503 Human MET
6	40	67.8	50	AAB50005	Aab50005 TSP1 doma
7	40	67.8	143	ABB11084	Abb11084 Human sec
8	40	67.8	157	AAB08133	Aab08133 Amino aci
9	40	67.8	170	ADL70644	Adl70644 Human thr
10	40	67.8	183	AAU74791	Aau74791 Human thr
11	40	67.8	218	AAW40287	Aaw40287 Human TSP
12	40	67.8	218	AAY06182	Aay06182 Thrombosp
13	40	67.8	239	AAR40823	Aar40823 Human thr
14	40	67.8	324	ADP04871	Adp04871 Sea squir
15	40	67.8	397	ADJ34131	Adj34131 Human sec
16	40	67.8	401	ADD18225	Add18225 Human mol
17	40	67.8	401	ADD18230	Add18230 Human mol
18	40	67.8	401	ADD18228	Add18228 Human mol
19	40	67.8	401	ADD18232	Add18232 Human mol
20	40	67.8	401	ADJ34125	Adj34125 Human sec
21	40	67.8	401	ADJ34123	Adj34123 Human sec
22	40	67.8	401	ADJ34121	Adj34121 Human sec
23	40	67.8	401	ADJ34127	Adj34127 Human sec
24	40	67.8	432	ADQ39359	Adq39359 Human myo
25	40	67.8	432	ADQ39357	Adq39357 Human myo

26	40	67.8	441	2	AAW40288	Aaw40288 Human con
27	40	67.8	441	2	AAY06183	Aay06183 Thrombosp
28	40	67.8	459	4	AAU02916	Aau02916 Angiotens
29	40	67.8	466	3	AAB43602	Aab43602 Human can
30	40	67.8	546	4	AAU02915	Aau02915 Angiotens
31	40	67.8	548	7	ADN02474	Adn02474 TSF polyp
32	40	67.8	555	4	AAU02914	Aau02914 Angiotens
33	40	67.8	606	5	ABG94994	Abg94994 Babesia a
34	40	67.8	606	8	ADP04709	Adp04709 Sea squir
35	40	67.8	731	4	AAU02913	Aau02913 Angiotens
36	40	67.8	939	5	AAG68296	Aag68296 Human sem
37	40	67.8	954	5	AAG68295	Aag68295 Human sem
38	40	67.8	999	3	AAY94990	Aay94990 Human sec
39	40	67.8	1034	5	AAG68291	Aag68291 Human sem
40	40	67.8	1049	5	AAG68289	Aag68289 Human sem
41	40	67.8	1078	5	AAG68292	Aag68292 Human sem
42	40	67.8	1092	5	ABG34077	Abg34077 Human PRO
43	40	67.8	1092	6	ADA01364	Ada01364 Human PRO
44	40	67.8	1092	6	ADA43793	Ada43793 Human sec
45	40	67.8	1092	6	ADA43561	Ada43561 Human sec

ALIGNMENTS

RESULT 1
AAR13629
ID AAR13629 standard; peptide; 23 AA.
XX
AC AAR13629;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-1991 (first entry)
XX
DE Thrombospondin peptide p11.
XX
KW Antiviral agent; wound healing; platelet aggregation; thrombotic;
KW thrombolytic.
XX
OS Synthetic.
XX
PN EP443404-A.
XX
PD 28-AUG-1991.
XX
PF 11-FEB-1991; 91EP-00101908.
XX
PR 22-FEB-1990; 90US-00483527.
PR 31-JAN-1991; 91US-00646531.
XX
(GRAC) GRACE & CO-CONN W R.
PA (MEDI-) MED COLLEGE OF PENNSYLVIA.
PA (DEUT/) DEUTCH A H.
XX
PI Deutch AH, Tuszynski GP;
XX
DR WPI; 1991-254044/35.
XX
PT New peptide fragments and analogues of thrombospondin - useful for
inhibiting tumour metastasis, as clotting agents and to promote or
inhibit cell adhesion and immune modulation.
PS Claim 3; Page 26; 30pp; English.
XX
CC The peptide is a synthetic fragment of human thrombospondin and is based
on the sequence motif of Robson et al (Nature (1988) 335:79- 82). It has
thrombospondin-like activity and can be used: (1) to inhibit tumour cell
metastasis and atherosclerosis; (2) to promote or nhbit platelet
aggregation, angiogenic activity, thrombotic or thrombolytic activity,
immune modulation and cell adhesion; (3) to promote wound healing; and (4)
as an antiviral agent (interferes with cell adhesion). The peptide is
prepd. by std. synthesis techniques. See also AAR13626-RL3641. (Updated
on 25-MAR-2003 to correct PA field.)

Fri Apr 1 15:03:06 2005

Best Local Similarity 50.0%; Pred. No. 11; Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

XX Sequence 23 AA;

Query Match 67.8%; Score 40; DB 2; Length 23; Best Local Similarity 50.0%; Pred. No. 11; Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
|||
Db 4 WSEWTSCSTSCG 15

RESULT 2
AAW81482
ID AAW81482 standard; peptide; 23 AA.

XX AC . AAW81482;
XX 29-JAN-1999 (first entry)
XX Thrombospondin synthetic analog compound p11.
XX Thrombospondin; thrombin sensitive protein; TSP; cell-adhesion;
KW mitogenic activity; chemotactic; haemostatic; tumour; microbial;
KW parasite; metastasis; platelet aggregation; fibrinolytic; malaria;
KW immune modulation; wound healing; atherosclerosis; angiogenesis;
KW complement modulator; diagnostic reagent.

XX Synthetic.

XX US5840692-A.

XX 24-NOV-1998.

XX 07-JUN-1995; 95US-00488273.

XX 22-FEB-1990; 90US-00483527.

XX 09-JUN-1992; 92US-00896527.

XX 20-AUG-1993; 93US-00110146.

XX 19-DEC-1994; 94US-00359263.

XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.

XX (GRAC) GRACE & CO-CONN W R.

XX Deutch AH, Tuszynski GP;

XX WPI; 1999-034078/03.

XX Method for mimicking or inhibiting thrombospondin activity - using thrombospondin peptides.

XX Claim 3; Col 29; 19pp; English.

XX Sequences AAW81478 to AAW81491 represent synthetic peptide analogs of thrombospondin (thrombin sensitive protein or TSP) that retain thrombospondin-like activity. The invention provides a method for (a) mimicking a biological activity of thrombospondin; (b) promoting thrombotic activity; or (c) inhibiting a biological activity of thrombospondin other than thrombotic activity. The method comprises administering any of these peptides. Biological activities of thrombospondin include cell adhesion-promoting activity, cell mitogenic activity, cell chemotactic activities, e.g. tumour-cell, microbial activities that derive from these activities, platelet aggregating activity, or parasite metastasis activity, immune modulation. The peptides are capable of inhibiting tumour metastasis. The peptides are useful in wound healing, atherosclerosis, malaria, thrombotic and thrombolytic conditions and angiogenesis, and as cell attachment promoters, complement modulators and diagnostic reagents

XX Sequence 23 AA;

XX Query Match 67.8%; Score 40; DB 2; Length 23;

QY 6 WSXXXCSXXCG 17
|||
Db 4 WSEWTSCSTSCG 15

RESULT 3
AAE20746
ID AAE20746 standard; peptide; 23 AA.

XX AAE20746;

XX 01-JUL-2002 (first entry)

XX Thrombospondin (TSP) peptide #13.

XX Thrombospondin; TSP; thrombin sensitive peptide; wound healing; cancer;
KW angiogenesis; tumour cell metastasis; anti-platelet aggregation; therapy;
KW malaria; thrombotic condition; atherosclerosis; rheumatoid arthritis;
KW vulnary; sickle cell disease; thrombocytopaenia; diabetic retinopathy;
KW cytostatic; protozoacide; haemostatic.

XX Unidentified.

XX US6339062-B1.

XX 15-JAN-2002.

XX 23-NOV-1998; 98US-00197770.

XX 23-NOV-1998; 98US-00197770.

XX (INKI-) INKINE PHARM CO INC.

XX Williams T, Tuszynski G, Actor P;

XX WPI; 2002-254234/30.

XX Novel polypeptide having retroinverso form of polypeptide that mimics/inhibits biological activity of thrombospondin, for treating cancer, malaria, wound healing, atherosclerosis, angiogenesis, thrombotic conditions.

XX Example 15; Col 11-12; 53pp; English.

XX The invention relates to a polypeptide having the retroinverso form of a polypeptide that mimics or inhibits the biological activity of thrombospondin (Thrombin sensitive peptide (TSP)), or a retroinverso polypeptide in which cysteine residues are modified with a sulphydryl blocking group. The polypeptide is useful for inhibiting tumour cell metastasis, invasion, adhesion and for inhibiting the invasive and metastatic activity of melanoma cells. The polypeptides are also useful for promoting and inhibiting cellular attachment to tissue culture flasks for promoting wound healing, angiogenesis and implant acceptance, as agents for anti-platelet aggregation and antimalarial activity, as diagnostic reagents in different therapeutic applications, in cancer therapy, for thrombotic and thrombolytic conditions, atherosclerosis, angiogenesis, for treating sickle cell disease states, for inhibiting thrombocytopaenia for inhibiting or preventing tumour growth, diabetic retinopathy and rheumatoid arthritis, as antiviral agents, as cell attachment promoters, complement modulators, and antimetastatic agents, in biomedical devices as a carrier to target toxins, drugs, hormones or imaging agents to metastatic tumour cells for diagnostic or therapeutic purposes, and to isolate thrombospondin cell surface receptors from extracts from cells or cell membranes. The present sequence is TSP peptide. Note: This sequence referred as TSP peptide (Seq ID NO: 13), found in column 11-12 does not match the corresponding sequence found in column 29-30 (AAE20781) of the specification

XX Sequence 23 AA;

Query Match 67.8%; Score 40; DB 5; Length 23;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
||| |||
Db 4 WSEWTSCTSCG 15

RESULT 4
ADM80537
ID ADM80537 standard; peptide; 23 AA.
XX
AC ADM80537;
XX
DT 03-JUN-2004 (first entry)
XX
DE Thrombospondin analogue peptide #11.
XX
KW thrombospondin; tumour cell metastasis; cell invasion; cell adhesion;
KW wound healing; implant acceptance; malaria; atherosclerosis; thrombosis.
XX
OS Synthetic.
XX
PN US2003171298-A1.
XX
PD 11-SEP-2003.
XX
PF 03-OCT-2001; 2001US-00042696.
XX
PR 23-NOV-1998; 98US-00197770.
XX
PA (INKI-) INKINE PHARM MCP HAHNEMANN.
XX
PI Williams T, Tuszynski G, Actor P;
XX
DR WPI; 2004-119157/12.
XX
PT New retroinverso polypeptide, useful for inhibiting tumor cell
PT metastasis, invasion or adhesion, for promoting wound healing or implant
PT acceptance, or for treating malaria, atherosclerosis or thrombosis.
XX
PS Claim 1; SEQ ID NO 11; 51pp; English.
XX
CC The invention relates to a polypeptide which has the retroinverso form of
CC a polypeptide which mimics or inhibits the biological activity of
CC thrombospondin. Also described is a method for inhibiting cell
CC metastasis, invasion or adhesion, comprising administering to a host the
CC retroinverso polypeptide compound. The retroinverso polypeptide is useful
CC for inhibiting tumour cell metastasis, invasion or adhesion, for
CC promoting wound healing or implant acceptance, or for treating malaria,
CC atherosclerosis or thrombosis. The present sequence represents a
CC thrombospondin analogue of the invention.

QY 6 WSXXXCSXXCG 17
||| |||
Db 4 WSEWTSCTSCG 15

RESULT 5
AA49503
ID AA49503 standard; protein; 50 AA.
XX
AC AA49503;
XX
DT 10-JAN-2000 (first entry)
XX

DE Human METH1 thombospondin-like domain #1.
XX
KW Human; METH1; METH2; anti-angiogenic; metalloprotease thrombospondin;
KW cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
KW angiogenesis inhibitor; abnormal wound healing; inflammation;
KW rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
KW diabetic retinopathy; macula degeneration; haemangioma; detection;
KW arterial-venous malformation; immune deficiency.
XX
OS Homo sapiens.
XX
PN WO9937660-A1.
XX
PD 29-JUL-1999.
XX
PF 22-JAN-1999; 99WO-US001313.
XX
PR 23-JAN-1998; 98US-0072298P.
PR 28-AUG-1998; 98US-0098539P.
XX
PA (TRUE/) IRUELA-ARISPE L.
PA (HAST/) HASTINGS G A.
PA (RUBE/) RUBEN S M.
XX
PI Iruela-Arispe L, Hastings GA, Ruben SM;
XX
DR WPI; 1999-590684/50.
XX
PT New isolated metalloprotease thrombospondin polypeptides, useful for
PT treating hyperproliferative disorders, cancers or autoimmune disorders.
XX
PS Disclosure; Fig 5; 457pp; English.
XX
CC AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human
CC metalloprotease thrombospondin (METH) proteins METH1 and METH2
CC respectively. METH1 and METH2 have been found to be potent inhibitors of
CC angiogenesis both in vitro and in vivo. They can be used for treating
CC cancer and other disorders related to angiogenesis including abnormal
CC wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial
CC bleeding disorders, diabetic retinopathy, some forms of macula
CC degeneration, haemangiomas, and arterial-venous malformations. They may
CC be useful in treating deficiencies or disorders of the immune system, by
CC activating or inhibiting the proliferation, differentiation, or
CC mobilisation (chemotaxis) of immune cells. The etiology of these immune
CC deficiencies or disorders may be genetic, somatic, such as cancer or some
CC autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or
CC infectious. They can also be used to treat inflammatory conditions, both
CC chronic and acute conditions. The products can also be used for detection
CC and diagnosis. AAZ32002 to AAZ32080, and AAY49503 to AAY49511 represent
CC sequences given in the exemplification of the present invention

QY Sequence 50 AA;
XX

Query Match 67.8%; Score 40; DB 2; Length 50;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXCSXXCG 17
||| |||
Db 7 WSEWTSCTSCG 18

RESULT 6
AAB50005
ID AAB50005 standard; protein; 50 AA.
XX
AC AAB50005;
XX
DT 19-MAR-2001 (first entry)
XX
DE TSP1 domain #1.
XX
KW Human; METH; metalloprotease; thrombospondin; angiogenesis inhibition;

Fri Apr 1 15:03:06 2005

KW cancer therapy; benign tumour; ocular angiogenic disease;
KW rheumatoid arthritis; psoriasis; wound healing; endometriosis;
KW vasculogenesis; granulation; hypertrophic scar; nonunion fracture;
KW scleroderma, trachoma; vascular adhesion; myocardial angiogenesis;
KW coronary collateral; cerebral collateral; arteriovenous malformation;
KW ischaemic limb angiogenesis; Osler-Webber syndrome; TSP domain;
KW plaque neovascularisation; telangiectasia; haemophilic joint;
KW angiofibroma; fibromuscular dysplasia; wound granulation;
KW Crohn's disease; atherosclerosis; birth control.
XX Homo sapiens.
OS WO200071577-A1.
XX 30-NOV-2000.
PD
XX 25-MAY-2000; 2000WO-US014462.
PF
XX 25-MAY-1999; 99US-00318208.
PR 20-JUL-1999; 99US-0144882P.
PR 10-AUG-1999; 99US-0147823P.
PR 13-AUG-1999; 99US-00373658.
PR 22-DEC-1999; 99US-0171503P.
PR 22-FEB-2000; 2000US-0183792P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA (IRUE/) IRUELA-ARISPE L.
PA (HAST/) HASTINGS G A.
PA (RUBE/) RUBEN S M.
PA (JONA/) JONAK Z L.
PA (TRUL/) TRULLI S H.
PA (FORN/) FORNWALD J A.
PA (TERR/) TERRETT J A.
XX Irue-la-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulli SH;
PI Fornwald JA, Terrett JA;
PI WPI; 2001-025136/03.
XX
XX METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit
PT angiogenesis in the treatment of disorders such as cancer, rheumatoid
PT arthritis and psoriasis.
XX
PS Disclosure; Fig 5; 768pp; English.
XX
XX The present invention relates to human METH1 and METH2, (ME for
CC metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).
CC The present sequence is a Tsp domain which are found in METH protein.
CC METH can be used for inhibiting angiogenesis in an individual, and for
CC treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid
CC arthritis, psoriasis, delayed wound healing, endometriosis,
CC vasculogenesis, granulations, hypertrophic scars, nonunion fractures,
CC scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
CC coronary collaterals, cerebral collaterals, arteriovenous malformations,
CC ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC fibromuscular dysplasia, wound granulation, Crohn's disease or
CC atherosclerosis. METH can also be used in birth control. METH can also be
CC used in diagnostic methods for the prognosis of cancer
XX
SQ Sequence 50 AA;

Query Match 67.8%; Score 40; DB 4; Length 50;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WXXXXCSXXCG 17
DB 7 WSEWTSCSTSCG 18

RESULT 7
ABB11084
ID ABB11084 standard; peptide; 143 AA.
XX
AC ABB11084;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human secreted protein homologue, SEQ ID NO:1454.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; anti-inflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.
XX Homo sapiens.
OS WO200157188-A2.
XX
PN 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US003800.
XX
XX 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-457740/49.
XX N-PSDB; ABA08328.
DR
XX Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 20; Page 144; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and

repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention

proteins are used for the treatment of conditions associated with angiogenesis and cancer. Angiogenic mediated diseases include tumours, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis), Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, neovascular glaucoma, retrolental fibroplasia, heliobacter related diseases, fractures, vasculogenesis, hematopoiesis, ovulation, menstruation and placentation. TRPs are also useful in the treatment of disease of excessive or abnormal stimulation of endothelial cells. TRP can also be used as a birth control agent, as it prevents the vascularisation required for embryo implantation

Fri Apr 1 15:03:06 2005

using the difference between (1) and (2) as a quantitation of the amount of TSP fragment or portion. Suitable epitopes are provided ADL70602-ADL70638. Detection or quantification of the TSP fragment or portion is performed in order to detect the presence, or monitor the course, of a disease or condition selected from cancer, renal failure, renal disease, atopic dermatitis, vasculitis, acute vasculitis, renal allograft, asthma, diabetes mellitus, myocardial infarction, liver disease, splenectomy, dermatomyositis, polyarteritis nodosa, systemic lupus erythematosus, lupus erythematosus, Kawasaki syndrome, non-specific vasculitis, juvenile rheumatoid arthritis, rheumatoid arthritis, vasculitis syndrome, Henoch-Schoenlein purpura, thrombocytopenic purpura, purpura, an inflammatory condition, a condition associated with clotting, a condition associated with platelet activation, a condition associated with intravascular platelet activation, a condition associated with consumption of platelets, heparin-induced thrombocytopenia, disseminated intravascular coagulation, intravascular coagulation, extravascular coagulation, a condition associated with endothelial activation, a condition associated with production and/or release of thrombospondin and/or a thrombospondin fragment, urticaria, hives, angioedema, a drug reaction, an antibiotic reaction, an aspartame reaction, atopic dermatitis, eczema, hypersensitivity, scleroderma, conditions associated with plugging of vessels, a condition associated with a cryofibrinogen, a condition associated with a cryoglobulin, and a condition associated with an anti-cardiolipin antibody. The cancer is selected from adenoma, adenocarcinoma, carcinoma, lymphoma, leukaemia, solid cancer, liquid cancer, metastatic cancer, pre-metastatic cancer, non-metastatic cancer, a cancer with vascular invasion, internal cancer, skin cancer, cancer of the respiratory system, circulatory system, musculoskeletal system, muscle, bone, a joint, tendon or ligament, digestive system, liver or biliary system, pancreas, head, neck, endocrine system, reproductive system (male or female), genitourinary system, kidney, urinary tract, sensory system, nervous system, lymphoid organ, blood, a gland, mammary gland, prostate gland, endometrial tissue, mesodermal tissue, ectodermal tissue, endodermal tissue, a teratoma, a poorly-differentiated cancer, a well-differentiated cancer or a moderately differentiated cancer.

Sequence 170 AA;

Query Match 67.8%; Score 40; DB 8; Length 170;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXXCG 17
||| ||| |||
Db 7 WSEWTSCTSCG 18

RESULT 10
AAU74791
ID AAU74791 standard; protein; 183 AA.

XX AC AAU74791;
XX DT 09-APR-2002 (first entry)
XX DE Human thrombospondin-1 (TSP-1) derived recombinant protein, 3TSR.
XX KW Thrombospondin-1; TSP-1; cytostatic; angiogenesis; vasotropic; vulnery;
KW neovascularisation; cell proliferation inhibitor; cancer; solid tumour;
KW haemangioma; acoustic neuromas; neurofibroma; trachoma;
KW pyogenic granulomas; rheumatoid arthritis; ocular angiogenic disease;
KW retinopathy; psoriasis; macular degeneration; corneal graft rejection;
KW neovascular glaucoma; retrolental fibroplasia; rebeosis; angiofibroma;
KW Osler-Webber syndrome; myocardial angiogenesis; haemophilic joints;
KW plaque neovascularisation; telangiectasia; wound granulation; apoptosis;
KW mutant; mutein; 3TSR.

XX OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1. .5
FT /label= Vector_derived_peptide

Protein 6. .175
/note= "Residues 361-530 of human thrombospondin-1 (TSP-1)"
Peptide 176. .183
/label= Vector_derived_peptide
WO200191781-A2.
06-DEC-2001.
25-MAY-2001; 2001WO-US017250.
26-MAY-2000; 2000US-0207994P.
(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
Lawler JW;
WPI; 2002-106273/14.

Composition useful for treatment of cancer comprises cDNA encoding amino acids of human thrombospondin-1 or its conservative variant and a carrier.

Example 1; Page; 54pp; English.

The invention describes a composition comprising cDNA encoding fragments of human thrombospondin-1 (TSP-1), a type 1 repeat polypeptide and potent inhibitor of tumour growth and angiogenesis. The composition is useful for killing cancerous cells (preferably tumour); for reducing volume or inhibiting growth of a tumour (inhibiting neovascularisation in the tumour); for decreasing proliferation of tumour cells; in the treatment of diseases and conditions associated with angiogenic activity or misregulated growth and angiogenesis-mediated diseases such as cancer, solid tumour, tumour metastasis, benign tumour, (e.g. haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas), rheumatoid arthritis, psoriasis, ocular angiogenic diseases (e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasias, rebeosis), Osler-Webber syndrome, myocardial angiogenesis, telangiectasia, plaque neovascularisation, haemophilic joints, angiofibroma or wound granulation. The composition induces apoptosis and inhibits neovascularisation in the tumour cells. This amino acid sequence represents a recombinant protein, 3TSR, derived from human thrombospondin-1 (TSP-1) and containing the 3 type 1 repeat (TSR) regions of TSP-1, described in the method of the invention. Note: This sequence does not appear in the specification but has been created using the human thrombospondin-1 (TSP-1) wild type sequence (see AAU74771) from information given in the invention

Sequence 183 AA;

Query Match 67.8%; Score 40; DB 5; Length 183;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXXCG 17
||| ||| |||
Db 12 WSEWTSCTSCG 23
RESULT 11
AAU40287
ID AAU40287 standard; protein; 218 AA.
XX AC AAU40287;
XX DT 18-AUG-1998 (first entry)
XX DE Human TSP1 protein.
XX KW TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy; liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;

Fri Apr 1 15:03:06 2005

OS Homo sapiens.
XX WO9316716-A1.
XX 02-SEP-1993.
XX 22-FEB-1993; 93WO-US001652.
XX 24-FEB-1992; 92US-00841656.
XX (NOUN) UNIV NORTHWESTERN.
XX Bouck NP, Polverini PJ, Good DJ, Frazier WA;
PI WPI; 1993-288118/36.
XX
XX Compn. for inhibiting angiogenesis - contg. a vascularisation inhibitor
PT comprising a peptide capable of inhibiting vascularisation.
XX
XX Claim 10; Page 41-42; 51pp; English.
XX
XX Certain fragments of thrombospondin, a glycoprotein found in the alpha
CC granules of platelets, can inhibit vascularisation. Peptides derived from
CC the hTSP sequence are useful for inhibiting neovascularisation, esp. in
CC solid tumours such as melanomas. The inhibitory peptides can also be used
CC in other diseases involving angiogenic dysfunction. See AAR40824-R40830.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 239 AA;

Query Match 67.8%; Score 40; DB 2; Length 239;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WSXXXXCSXXCG 17
Db 74 WSEWTSCSTSCG 85
||| ||| |||
||| ||| |||

RESULT 14
ADP04871
ID ADP04871 standard; protein; 324 AA.
XX
AC ADP04871;
XX
DT 29-JUL-2004 (first entry)
XX
DE Sea squirt protein with tissue specific expression in development Seq#66.
XX
KW sea squirt; regeneration medicine; gene therapy; cell proliferation;
KW differentiation; reproduction; environmental measurement; water survey.
XX
OS Ciona intestinalis.
XX
PN JP2004057129-A.
XX
PD 26-FEB-2004.
XX
PF 31-JUL-2002; 2002JP-00222593.
XX
PR 31-JUL-2002; 2002JP-00222593.
XX
PR (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
PA WPI; 2004-287079/27.
XX
DR N-PSDB; ADP04870.
XX
XX Novel gene cluster which is specifically expressed in tissue or organ
PT during developmental phase of sea squirt, useful for elucidation of
PT mechanism of development of tissue or organ of sea squirt.
XX
PS Claim 1; SEQ ID NO 466; 1846pp; Japanese.
XX

CC This invention relates to novel genes and the encoded proteins thereof
CC that are derived from the sea squirt Ciona intestinalis. Specifically, it
CC refers to those genes that are expressed in the tissues or organs of the
CC sea squirt during its developmental phase. The present invention
CC describes the identification of these genes as useful for elucidation of
CC the mechanism of development and hence for developing regeneration
CC medicines and gene therapy techniques. Accordingly, they can be used in
CC the research of various genetic diseases, as well as the analysis of cell
CC proliferation, differentiation and reproduction. Furthermore, such
CC compositions can be useful for environmental measurements and water
CC surveys, particularly for sea water surveys, and also for the preparation
CC of transformed sea squirt for improving edibility of sea squirt such as
CC Halocynthia roretzi. This polypeptide sequence is a sea squirt protein
CC sequence that has tissue specific expression during development, given in
CC an exemplification of the invention.
XX
XX Sequence 324 AA;

Query Match 67.8%; Score 40; DB 8; Length 324;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 WSXXXXCSXXCG 17
Db 85 WSSWSRCSSSCG 96
||| ||| |||
||| ||| |||

RESULT 15
ADJ34131
ID ADJ34131 standard; protein; 397 AA.
XX
AC ADJ34131;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human secreted protein NOV2h.
XX
KW Human; NOVX; secreted protein; cancer; diabetes; obesity;
KW endocrine disorder; CNS disorder; inflammatory disorder; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2004000997-A2.
XX
PD 31-DEC-2003.
XX
PF 04-JUN-2003; 2003WO-US017512.
XX
PR 19-MAR-2002; 2002US-0365491P.
PR 04-JUN-2002; 2002US-0385504P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386974P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0387002P.
PR 10-JUN-2002; 2002US-0387540P.
PR 11-JUN-2002; 2002US-0387659P.
PR 12-JUN-2002; 2002US-0387934P.
PR 13-JUN-2002; 2002US-0389123P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 19-JUN-2002; 2002US-0390066P.
PR 17-JUL-2002; 2002US-0396706P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403486P.
PR 14-AUG-2002; 2002US-0403522P.
PR 15-AUG-2002; 2002US-0403748P.
PR 06-NOV-2002; 2002US-0387037P.
PR 03-JUN-2003; 2003US-00454246.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Anderson DW, Boldog FL, Burgess CE, Casman SJ, Edinger SR;

PI Eisen A, Ellerman K, Gerlach VL, Gorman L, Guo X, Gusev VY, Ji W;
PI Li L, Macdougall JR, Malyankar UM, Millet I, Ort T, Padigar M;
PI Prayaga SK, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Sciore P, Shenoy SG, Smithson G, Spytek KA, Stone DJ;
PI Taupier RJ, Tchernev VT, Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
XX
DR WPI; 2004-082483/08.
DR N-PSDB; ADJ34130.
XX
PT New isolated NOVX polypeptides useful for treating, preventing and
PT diagnosing pathological conditions with NOVX-associated disorders, such
PT as cancer, obesity, diabetes and inflammatory or CNS diseases.
XX
PS Claim 1; SEQ ID NO 20; 418pp; English.
XX
CC The invention relates to a new isolated polypeptide (designated NOVX)
CC comprising one of 141 fully defined sequences, their mature forms, a
CC protein comprising one or more conservative substitutions or having at
CC least 95% identity to one of the 141 proteins. Also included are a
CC composition comprising NOVX (or a NOVX nucleic acid molecule (NA)), a kit
CC comprising the composition of NOVX in one or more containers, an isolated
CC nucleic acid molecule encoding a NOVX protein, producing NOVX (comprising
CC culturing a cell under conditions that lead to expression of the
CC polypeptide, where the cell comprises a vector comprising NOVX NA),
CC identifying an agent that binds to NOVX, identifying a potential
CC therapeutic agent for use in the treatment of a pathology that is related
CC to aberrant expression or physiological interactions of NOVX, screening
CC for a modulator of activity of or latency or predisposition to a
CC pathology associated with NOVX, modulating the activity of NOVX, treating
CC or preventing a pathology associated with NOVX, treating a pathological
CC state in a mammal, a vector comprising the NOVX nucleic acid molecule, a
CC cell comprising the vector, an antibody that immunospecifically binds to
CC NOVX, determining the presence or amount of NOVX or the nucleic acid
CC molecule in a sample, and determining the presence of or predisposition
CC to a disease associated with altered levels of expression of NOVX or the
CC nucleic acid molecule in a first mammalian subject. The methods and
CC compositions of the present invention are useful for the diagnosis and
CC treatment of disorders associated with aberrant expression or activity of
CC the NOVX polypeptide, such as cancer, diabetes, obesity, and endocrine,
CC CNS and inflammatory disorders. They can also be used in various
CC detection and screening assays, chromosome mapping, tissue typing, gene
CC therapy and predictive medicine. The present sequence represents a NOVX
CC protein.
XX
SQ Sequence 397 AA;

Query Match 67.8%; Score 40; DB 8; Length 397;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 WSXXXXCSCXCG 17
|||
Db 58 WSSWALCSTSCG 69

Search completed: April 1, 2005, 13:54:27
Job time : 154.522 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:24:31 ; Search time 75.6522 Seconds
(without alignments)
81.226 Million cell updates/sec

Title: US-09-462-909D-8
Perfect score: 77
Sequence: 1 WSGWSSCSRSCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	77	100.0	867	1	SSPO BOVIN	P98167 bos taurus
2	77	100.0	5146	2	Q8SPM4	Q8SPM4 bos taurus
3	73	94.8	4998	2	Q8CG65	Q8CG65 mus musculus
4	73	94.8	5141	2	Q700K0	Q700K0 rattus norv
5	70	90.9	880	2	Q8MSF8	Q8MSF8 drosophila
6	70	90.9	880	2	Q9VKV3	Q9VKV3 drosophila
7	67	87.0	168	2	Q9GZ21	Q9GZ21 cryptospori
8	67	87.0	1088	2	Q6PCK8	Q6PCK8 xenopus lae
9	67	87.0	1361	2	Q6PD18	Q6PD18 mus musculus
10	67	87.0	1461	2	Q8MYA8	Q8MYA8 caenorhabdi
11	67	87.0	1641	2	Q68SA9	Q68SA9 mus musculus
12	66	85.7	1637	2	Q9XSV8	Q9XSV8 bos taurus
13	65	84.4	125	2	Q7Z292	Q7Z292 caenorhabdi
14	65	84.4	238	2	Q76510	Q76510 cryptospori
15	65	84.4	685	2	Q9TTS5	Q9TTS5 bos taurus
16	65	84.4	769	2	Q8MRL5	Q8MRL5 drosophila
17	65	84.4	975	2	Q7Z291	Q7Z291 caenorhabdi
18	65	84.4	988	2	Q7PWY7	Q7PWY7 anopheles g
19	65	84.4	997	1	ATS7 HUMAN	Q9UKP4 homo sapien
20	65	84.4	1020	2	Q19204	Q19204 caenorhabdi
21	65	84.4	1020	2	Q8IU50	Q8IU50 caenorhabdi
22	65	84.4	1059	2	Q9W493	Q9W493 drosophila
23	65	84.4	1686	2	Q6P7J9	Q6P7J9 homo sapien
24	65	84.4	3869	2	Q86PQ3	Q86PQ3 cryptospori
25	64	83.1	257	2	Q966K7	Q966K7 caenorhabdi
26	64	83.1	1089	2	Q8T3A0	Q8T3A0 ciona intes
27	64	83.1	2098	2	Q25757	Q25757 plasmodium
28	64	83.1	2114	2	O97267	O97267 halocynthia
29	63	81.8	415	2	O44228	O44228 mus musculus
30	63	81.8	1210	1	AT19_MOUSE	P59509 mus musculus
31	63	81.8	1224	1	AT16_HUMAN	Q8TE57 homo sapien

32	63	81.8	1502	2	Q9UPZ6	Q9UPZ6 homo sapien
33	63	81.8	1668	2	Q69ZU6	Q69ZU6 mus musculus
34	63	81.8	2401	2	Q7RF52	Q7RF52 plasmodium
35	62	80.5	504	2	Q69HL7	Q69HL7 ciona intes
36	62	80.5	808	2	O42113	O42113 brachydanio
37	62	80.5	1081	1	AT18_HUMAN	Q8TE60 homo sapien
38	62	80.5	1092	2	O8BKA1	Q8BKA1 mus musculus
39	62	80.5	1221	2	Q6P4R5	Q6P4R5 homo sapien
40	61	79.2	129	2	Q8IVU0	Q8IVU0 homo sapien
41	61	79.2	551	1	YVD3_CABEL	P55114 caenorhabdi
42	61	79.2	803	2	O42114	O42114 brachydanio
43	61	79.2	872	2	Q22580	Q22580 caenorhabdi
44	61	79.2	900	2	Q8K206	Q8K206 mus musculus
45	61	79.2	1009	2	Q8BKY1	Q8BKY1 m mus muscu

ALIGNMENTS

RESULT 1
SSPO_BOVIN
ID SSPO_BOVIN STANDARD; PRT; 867 AA.
AC P98167;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE SCO-spondin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ependymocyte;
RX MEDLINE=96338614; PubMed=8743952;
RA Gobron S., Monnerie H., Meinie R., Creveaux I., Lehmann W.,
RA Lamalle D., Dastugue B., Meinie A.;
RT "SCO-spondin: a new member of the thrombospondin family secreted by
RT the subcommissural organ is a candidate in the modulation of neuronal
RT aggregation.";
RL J. Cell Sci. 109:1053-1061(1996).
CC -1- FUNCTION: Involved in the modulation of neuronal aggregation.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Subcommissural organ.
CC -1- DEVELOPMENTAL STAGE: Embryo.
CC -1- SIMILARITY: Belongs to the thrombospondin family.
CC -1- SIMILARITY: Contains at least 2 EGF-like domains.
CC -1- SIMILARITY: Contains at least 1 FS/8 type C domain.
CC -1- SIMILARITY: Contains at least 3 LDL-receptor class A domains.
CC -1- SIMILARITY: Contains at least 4 TSP type-1 domains.
CC -1- SIMILARITY: Contains 1 VWFC domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X93922; CAA63815.1; --
CC HSSP; P01130; 1AJJ.
CC InterPro; IPR002919; Cysrich_TIL.
CC InterPro; IPR000421; FA58 C.
CC InterPro; IPR008979; Gal_Bind like.
CC InterPro; IPR002172; LDL_receptor_A.
CC InterPro; IPR009041; PMP_SGCI.
CC InterPro; IPR000884; TSP1.
CC InterPro; IPR008085; TSP_1.
CC InterPro; IPR001007; VWFC.
CC Pfam; PF00754; F5_F8_type_C; 1.
CC Pfam; PF00057; Ldl_recept_a; 3.

DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00090; TSP_1; 4.
DR Pfam; PF00093; WVC; 1.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PRINTS; PR01705; TSP1REPEAT.
DR PROSITE; PS01285; FA58C_1; 1.
DR PROSITE; PS01286; FA58C_2; 1.
DR PROSITE; PS00022; FA58C_3; 1.
DR PROSITE; PS01209; LDLRA_1; 3.
DR PROSITE; PS00068; LDLRA_2; 3.
DR PROSITE; PS00092; TSP1; 4.
DR PROSITE; PS0184; WVC_2; 1.
KW Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein; Repeat.
FT NON_TER 1 87
FT DOMAIN 29 87 TSP type-1 1.
FT DOMAIN 103 142 EGF-like 1.
FT DOMAIN 143 180 EGF-like 2.
FT DOMAIN 188 244 TSP type-1 2.
FT DOMAIN 245 304 WVC.
FT DOMAIN 344 502 F5/8 type C.
FT DOMAIN 506 544 LDL-receptor class A 1.
FT DOMAIN 663 701 LDL-receptor class A 2.
FT DOMAIN 723 761 LDL-receptor class A 3.
FT DOMAIN 761 814 TSP type-1 3.
FT DOMAIN 816 866 TSP type-1 4.
FT DISULFID 107 122 By similarity.
FT DISULFID 116 127 By similarity.
FT DISULFID 129 141 By similarity.
FT DISULFID 147 166 By similarity.
FT DISULFID 149 169 By similarity.
FT DISULFID 171 179 By similarity.
FT DISULFID 344 502 By similarity.
FT DISULFID 508 520 By similarity.
FT DISULFID 515 533 By similarity.
FT DISULFID 527 542 By similarity.
FT DISULFID 665 677 By similarity.
FT DISULFID 672 690 By similarity.
FT DISULFID 684 699 By similarity.
FT DISULFID 725 737 By similarity.
FT DISULFID 732 750 By similarity.
FT DISULFID 744 759 By similarity.
FT CARBOHYD 88 88 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 309 309 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 409 409 N-linked (GlcNAc. . .) (Potential).
FT NON_TER 867 867
SQ SEQUENCE 867 AA; 91817 MW; 9538F2108E787B49 CRC64;
Query Match 100.0%; Score 77; DB 1; Length 867;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
Db 767 WSGWSSCSRSCG 778
RESULT 2
Q8SPM4 PRELIMINARY; PRT; 5146 AA.
AC Q8SPM4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SCO-spondin.
GN Name=sco-spondin;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Subcommissural organ;

RX MEDLINE=20465125; PubMed=11008217;
RX DOI=10.1002/1098-1136(200011)32:2<177::AID-GLIA70>3.0.CO;2-V;
RA Gobron S.;
RT "Subcommissural organ/Reissner's fiber complex: characterization of
RT SCO-spondin, a glycoprotein with potent activity on neurite
RT outgrowth.";
RL Glia 32:177-191(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Subcommissural organ;
RA Meinzel A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ16457; CAC94914.1; -.
DR HSSP; P98162; 1K7B.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0030414; F:protease inhibitor activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR008037; Prot_inh_PMP.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; Ldl_recept_a; 10.
DR Pfam; PF05375; Pacifastin_I; 1.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP_1; 25.
DR Pfam; PF00093; WVC; 1.
DR Pfam; PF00094; WVD; 3.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00041; CT; 1.
DR SMART; SM00231; FA58C_1.
DR SMART; SM00068; GHB; 1.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSP1; 25.
DR SMART; SM00214; WVC; 3.
DR SMART; SM00216; WVD; 3.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01285; FA58C_1; UNKNOWN_1.
DR PROSITE; PS01286; FA58C_2; 1.
DR PROSITE; PS00022; FA58C_3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 2.
DR PROSITE; PS01209; LDLRA_1; 7.
DR PROSITE; PS00068; LDLRA_2; 9.
DR PROSITE; PS00092; TSP1; 25.
DR PROSITE; PS01208; WVC_1; UNKNOWN_1.
DR PROSITE; PS0184; WVC_2; 2.
DR PROSITE; PS0184; WVC_2; 2.
SQ SEQUENCE 5146 AA; 543588 MW; 724C5FB8727E13DA CRC64;

Query Match 100.0%; Score 77; DB 2; Length 5146;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
Db 2485 WSGWSSCSRSCG 2496

RESULT 3
Q8CG65 PRELIMINARY; PRT; 4998 AA.
ID Q8CG65
AC Q8CG65;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE SCO-spondin.
GN Name=Scospondin; Synonyms=sco-spondin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Goncalves N., Simon-Chazottes D., Creveaux I., Meinzel A.,
RA Guenet J.-L., Meinzel R.;
RT "Mouse SCO-spondin, a gene of the thrombospondin type 1 repeat (TSR)
RT superfamily expressed in the brain.";
RL Gene 312:263-270(2003).
CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ491857; CAD42654.1; -.
DR HSSP; P01130; 1AJJ.
DR MGD; MGI:2674311; Scospondin.
DR GO; GO:0005737; C:cytoplasm; IC.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR008037; Prot_inh_PMP.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; Ldl_recept_a; 10.
DR Pfam; PF05375; Pacifastin_I; 1.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP_1; 25.
DR Pfam; PF00093; VWC; 1.
DR Pfam; PF00094; VWD; 2.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PRINTS; PR01705; TSPIREPEAT.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00068; GHB; 1.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSP1; 25.
DR SMART; SM00214; VWC; 4.
DR SMART; SM00216; VWD; 2.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00022; FA58C_3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 10.
DR PROSITE; PS50092; TSP1; 25.
DR PROSITE; PS01208; VWF_C_1; UNKNOWN_1.
DR PROSITE; PS50184; VWF_C_2; 2.
SQ SEQUENCE 4998 AA; 535028 MW; DA2ABA8DA47DF225 CRC64;

Query Match 94.8%; Score 73; DB 2; Length 4998;
Best Local Similarity 91.7%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 2342 WSGWSDCSRSCG 2353

RESULT 4
Q700K0
ID Q700K0 PRELIMINARY; PRT; 5141 AA.
AC Q700K0;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SCO-spondin.
GN Name=sco-spondin; (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Meinzel O.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ629845; CAF33425.1; -.
DR HSSP; P01130; 1AJJ.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR006552; VWC_out.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; Ldl_recept_a; 8.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP_1; 25.
DR Pfam; PF00093; VWC; 1.
DR Pfam; PF00094; VWD; 3.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSP1; 25.
DR SMART; SM00214; VWC; 5.
DR SMART; SM00215; VWC_out; 9.
DR SMART; SM00216; VWD; 3.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS00022; FA58C_3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 10.
DR PROSITE; PS50092; TSP1; 24.
DR PROSITE; PS01208; VWF_C_1; UNKNOWN_1.
DR PROSITE; PS50184; VWF_C_2; 2.
SQ SEQUENCE 5141 AA; 550644 MW; 1772AE67F02CA5E3 CRC64;

Query Match 94.8%; Score 73; DB 2; Length 5141;
Best Local Similarity 91.7%; Pred. No. 0.21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 2491 WSGWSDCSRSCG 2502

RESULT 5
Q8MSF8
ID Q8MSF8 PRELIMINARY; PRT; 880 AA.
AC Q8MSF8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GMI5606p.
GN ORFNames=CG6232;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Fri Apr 1 15:03:06 2005

OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY118849; AAM50709.1; --
DR HSSP; P07996; 1LSL.
DR FlyBase; FBgn0032252; CG6232.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00090; TSP_1; 3.
DR SMART; SM00209; TSPI; 6.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSPI; 5.
SQ SEQUENCE 880 AA; 98882 MW; FB3FAAD5B54106CE CRC64;

Query Match 90.9%; Score 70; DB 2; Length 880;
Best Local Similarity 91.7%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSRG 12
Db 185 WSDWSSCSRSRG 196

RESULT 6
Q9VKV3 PRELIMINARY; PRT; 880 AA.
ID Q9VKV3
AC Q9VKV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6232-PA.
GN ORFNames=CG6232;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.N., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.S., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003628; AAF52956.3; --
DR FlyBase; FBgn0032252; CG6232.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00090; TSP_1; 3.
DR SMART; SM00209; TSPI; 4.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSPI; 3.
SQ SEQUENCE 880 AA; 99015 MW; E42DF10B56560B25 CRC64;

Query Match 90.9%; Score 70; DB 2; Length 880;
Best Local Similarity 91.7%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 WSGWSSCSRSCG 12
Db 185 WSDWSSCSRSCG 196

RESULT 7
Q9GZ21 PRELIMINARY; PRT; 168 AA.
AC
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium meleagridis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=93969;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20389602; PubMed=10930736;
RA Pedraza-Diaz S., Amar C., McLauchlin J.;
RT "The identification and characterisation of an unusual genotype of
RT Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
RL FEMS Microbiol. Lett. 189:189-194 (2000).
DR EMBL; AF248746; AAG01095.1; -.
DR HSSP; P07996; 1LSL.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP 1; 2.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 18576 MW; CE9516EEE86479C3 CRC64;

Query Match 87.0%; Score 67; DB 2; Length 168;
Best Local Similarity 83.3%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
Db 85 WSGWSDCSTSCG 96

RESULT 8
Q6PCK8 PRELIMINARY; PRT; 1088 AA.
AC
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68835 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC059288; AAH59288.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003659; P:development; IEA.
DR InterPro; IPR002165; Plexin-like.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP 1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 6.
DR PROSITE; PS50092; TSP1; 6.
SQ SEQUENCE 1088 AA; 122657 MW; 4DFCD371A7CD8176 CRC64;

Query Match 87.0%; Score 67; DB 2; Length 1088;
Best Local Similarity 90.9%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSC 11
Db 797 WSGWSSCSRDC 807

RESULT 9
Q6PD18 PRELIMINARY; PRT; 1361 AA.
AC
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Adamts7 protein (Fragment).
GN Name=Adamts7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058991; AAS58991.1; -.
DR HSSP; P15167; IATL.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP1.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP1; 6.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00209; TSP1; 7.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 6.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 1361 AA; 149549 MW; 49D04B6A28AFA877 CRC64;

Query Match 87.0%; Score 67; DB 2; Length 1361;
Best Local Similarity 83.3%; Pred. No. 0.44;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||| ||| ||| |||
Db 277 WSAWSDCSRSCG 288

RESULT 10
Q8MYA8 PRELIMINARY; PRT; 1461 AA.
AC Q8MYA8; Q17591; Q22300;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ADT-1 (Hypothetical protein C02B4.1).
GN Name=adt-1; ORFNames=C02B4.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kuno K., Baba C., Asaka A., Hosono R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology";
RL Science 282:2012-2018(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurray A.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB066246; BAC05514.1; -.
DR EMBL; Z50004; CAA90293.2; -.
DR EMBL; Z50006; CAA90293.2; JOINED.
DR EMBL; Z50004; CAA90302.2; JOINED.
DR EMBL; Z50006; CAA90302.2; -.
DR HSSP; P07996; ILSL.
DR MEROPS; M12.302; -.
DR WormBase; WBGene0000082; adt-1.
DR WormPep; C02B4.1; CE31872.
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP1; 12.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 13.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50092; TSP1; 12.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 1461 AA; 162615 MW; 3CFDC1C07C1F493A CRC64;

Query Match 87.0%; Score 67; DB 2; Length 1461;
Best Local Similarity 83.3%; Pred. No. 0.47;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||| ||| ||| |||
Db 1088 WSDWSSCSRSCG 1099

RESULT 11
Q68SA9 PRELIMINARY; PRT; 1641 AA.
ID Q68SA9
AC Q68SA9;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE ADAMTS7B.
GN Name=Adamts7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15192113; DOI=10.1074/jbc.M402380200;
RA Somerville R.P.T., Longpre J.M., Apel E.D., Lewis R.M., Wang L.W.,
RA Sanes J.R., Leduc R., Apte S.S.;
RT "ADAMTS7B, the full-length product of the ADAMTS7 gene, is a
chondroitin sulfate proteoglycan containing a mucin domain";
RL J. Biol. Chem. 279:35159-35175(2004).
DR EMBL; AY551090; AAT36307.1; -.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP1.
DR Pfam; PF05986; ADAM_spacer1; 1.

DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysins; 1.
DR Pfam; PF00090; TSP_1; 6.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00209; TSP1; 8.
DR PROSITE; PS02015; ADAM_MEPRO; 1.
DR PROSITE; PS50092; TSP1; 6.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 1641 AA; 180743 MW; BA3E1E7B492D6165 CRC64;

Query Match 87.0%; Score 67; DB 2; Length 1641;
Best Local Similarity 83.3%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 529 WSAWSDCSRSCG 540

RESULT 12
Q9XSV8 PRELIMINARY; PRT; 1637 AA.
AC Q9XSV8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SCO-spondin (Fragment).
GN Name=sco-spondin;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gobron S., Creveaux I., Didier R., Meinzel R.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133488; CAB46239.1; -.
DR HSSP; P07996; 1LSL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR009041; PMP_SGCI.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF01826; TIL; 3.
DR Pfam; PF00090; TSP_1; 11.
DR Pfam; PF00093; VWC; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00068; GHB; 1.
DR SMART; SM00209; TSP1; 11.
DR SMART; SM00214; VWC; 2.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00261; GLYC_HORMONE_BETA_1; 2.
DR PROSITE; PS50092; TSP1; 11.
DR PROSITE; PS01208; VWF_C_1; UNKNOWN_1.
DR PROSITE; PS50184; VWF_C_2; 1.
FT NON TER 1
SQ SEQUENCE 1637 AA; 173346 MW; 4C5BAB1DD346C925 CRC64;

Query Match 85.7%; Score 66; DB 2; Length 1637;
Best Local Similarity 83.3%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 648 WSAWSDCSRSCG 659

RESULT 13
Q7Z292 PRELIMINARY; PRT; 125 AA.
AC Q7Z292;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Adamts family protein 2, isoform b.
GN Name=adt-2; ORFNames=F08C6.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid F08C6.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U29378; AAP40540.1; -.
DR WormBase; WBGene0000083; adt-2.
DR WormPep; F08C6.1b; CE33991.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 2.
DR SMART; SM00209; TSP1; 2.
DR PROSITE; PS50092; TSP1; 2.
SQ SEQUENCE 125 AA; 13940 MW; C572F021DE87A468 CRC64;

Query Match 84.4%; Score 65; DB 2; Length 125;
Best Local Similarity 83.3%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 26 WSGWSDCSRSCG 37

RESULT 14
Q76510 PRELIMINARY; PRT; 238 AA.
AC Q76510;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C3;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.

Search completed: April 1, 2005, 13:59:23

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:43:07 ; Search time 16.6957 Seconds
(without alignments)
69.156 Million cell updates/sec

Title: US-09-462-909D-8
Perfect score: 77
Sequence: 1 WSGWSSCSRSCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: PIR: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	87.0	1444	2 T18856	angiogenesis inhib
2	65	84.4	957	2 T15976	hypothetical prote
3	64	83.1	2098	2 T18397	protein CTRP - mal
4	61	79.2	551	2 T16557	hypothetical prote
5	61	79.2	860	2 T16892	hypothetical prote
6	61	79.2	1572	2 T00027	brain-specific ang
7	60	77.9	1059	2 T22545	hypothetical prote
8	60	77.9	1170	1 TSHUP1	thrombospondin 1 p
9	59	76.6	807	2 A38152	F-spondin - rat
10	58	75.3	654	2 T29247	hypothetical prote
11	58	75.3	803	2 A47723	F-spondin precurs
12	58	75.3	1170	2 A40558	thrombospondin 1 p
13	58	75.3	1172	1 TSHUP2	thrombospondin 2 p
14	58	75.3	1172	2 A42587	thrombospondin 2 p
15	58	75.3	1178	1 A39804	hypothetical prote
16	57	74.0	651	2 T19477	thrombospondin pre
17	57	74.0	724	2 A48569	antigen Em100 - Ei
18	56	72.7	788	2 T25061	hypothetical prote
19	56	72.7	805	2 T34212	hypothetical prote
20	56	72.7	1184	2 T09484	cartilage intermed
21	56	72.7	1584	2 T00026	brain-specific ang
22	55	71.4	919	2 T32541	unc-5 protein - Ca
23	55	71.4	947	1 B44294	unc-5 protein, lon
24	55	71.4	984	2 T00326	hypothetical prote
25	55	71.4	1522	2 T00028	brain-specific ang
26	55	71.4	2165	2 T21371	hypothetical prote
27	54	70.1	550	2 T47158	hypothetical prote
28	54	70.1	610	2 T16761	hypothetical prote
29	54	70.1	837	2 T00355	hypothetical prote

30	54	70.1	951	2 T00017	gene ADAMTS-1 prot
31	54	70.1	1074	2 JC5928	semaphorin F precu
32	53	68.8	206	2 A45517	coccidiosis-relate
33	53	68.8	712	2 A45638	immunodominant mic
34	53	68.8	736	2 T19366	hypothetical prote
35	53	68.8	951	2 T00260	hypothetical prote
36	52.5	68.2	1205	2 T18517	procollagen N-endo
37	52	67.5	123	2 S49108	TRAP-C2 protein -
38	52	67.5	898	2 T14764	hypothetical prote
39	52	67.5	1360	2 T33922	hypothetical prote
40	51	66.2	934	1 A34372	complement C6 prec
41	51	66.2	2761	2 T21064	hypothetical prote
42	50	64.9	351	2 S20078	NOV protein - chic
43	50	64.9	379	2 A35669	gene CYR61 protein
44	49	63.6	324	2 T32570	hypothetical prote
45	49	63.6	559	2 S04531	thrombospondin-rel

ALIGNMENTS

RESULT 1

T18856
angiogenesis inhibitor homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18856; T24653
R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19031

A;Accession: T18856

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WIL>

A;Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN000028; CESP:CO2

A;Experimental source: clone C02B4

R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19917

A;Accession: T24653

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WI2>

A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN000028; CESP:CO2B4.1

A;Experimental source: clone T07C5

C;Genetics:

A;Gene: CESP:C02B4.1

A;Map position: X

A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/

Query Match 87.0%; Score 67; DB 2; Length 1444;
Best Local Similarity 83.3%; Pred. No. 0.12;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

|| |||||: |||

Db 1071 WSDWSSCSKSCG 1082

RESULT 2

T15976

hypothetical protein F08C6.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T15976

R;Bentley, D.

submitted to the EMBL Data Library, June 1995

A;Description: The sequence of C. elegans cosmid F08C6.

A;Reference number: Z18440

A;Accession: T15976

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-957 <BEN>

C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16892
R;Bentley, D.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19D2.
A;Reference number: Z18599
A;Accession: T16892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-860 <BEN>
A;Cross-references: UNIPROT:Q22580; EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA8360
C;Genetics:
A;Gene: CESP:T19D2.1
A;Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 582/3

Query Match 79.2%; Score 61; DB 2; Length 860;
Best Local Similarity 75.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||||| ||
Db 831 WSSWSSCTKCG 842

RESULT 6
T00027
brain-specific angiogenesis inhibitor 2 - human
N;Alternate names: BAI2 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00027
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cytoget. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to brain-
A;Reference number: Z14066; MUID:98194217; PMID:9533023
A;Accession: T00027
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1572 <SHI>
A;Cross-references: UNIPROT:O60241; EMBL:AB005298; NID:g3021698; PIDN:BAA25362.1; PID:g3021698
A;Experimental source: brain
C;Genetics:
A;Gene: GDB:BAI2
A;Cross-references: GDB:9838089; OMIM:602683
A;Map position: lp35-lp35

Query Match 79.2%; Score 61; DB 2; Length 1572;
Best Local Similarity 75.0%; Pred. No. 0.85;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||||| ||
Db 358 WGSWSLCSRSCG 369

RESULT 7
T22545
hypothetical protein F53B6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22545
R;White, S.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19578
A;Accession: T22545
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1059 <WIL>
A;Cross-references: UNIPROT:P90884; EMBL:Z81086; PIDN:CAB03121.1; GSPDB:GN00019; CESP:F53B6
A;Experimental source: clone F53B6
C;Genetics:
A;Gene: CESP:F53B6.2

C;Cross-references: UNIPROT:Q19204; EMBL:U29378; NID:g868184; PID:g868185; PIDN:AAA68721
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F08C6.1
A;Introns: 23/1; 135/3; 220/3; 285/3; 325/2; 376/3; 461/2; 498/3; 532/3; 627/2; 714/1; 714/1

Query Match 84.4%; Score 65; DB 2; Length 957;
Best Local Similarity 83.3%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||||| ||
Db 858 WSGWSQCSVSCG 869

RESULT 3
T18397
protein CTBP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397
R;Trottein, F.; Trigilia, T.; Cowman, A.F.
Mol. Biochem. Parasitol. 74, 129-142, 1995
A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein
A;Reference number: Z18926; MUID:96360471; PMID:8719155
A;Accession: T18397
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2098 <TRO>
A;Cross-references: UNIPROT:Q25757; EMBL:U34363; NID:g1098897; PID:g1098898; PIDN:AAC469

Query Match 83.1%; Score 64; DB 2; Length 2098;
Best Local Similarity 75.0%; Pred. No. 0.42;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||||| ||
Db 1644 WSDWSSCKTCG 1655

RESULT 4
T16557
hypothetical protein K04E7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16557
R;Nhan, M.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid K04E7.
A;Reference number: Z18535
A;Accession: T16557
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-551 <NHA>
A;Cross-references: UNIPROT:P55114; EMBL:U39666; NID:g1049408; PID:g1049411; PIDN:AAA804
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:K04E7.3
A;Introns: 43/3; 81/3; 112/3; 153/1; 191/2; 213/3; 241/2; 281/3; 324/1; 364/1; 393/3; 411/3

Query Match 79.2%; Score 61; DB 2; Length 551;
Best Local Similarity 66.7%; Pred. No. 0.39;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||||| ||
Db 491 WSGWTRCSENCG 502

RESULT 5
T16892
hypothetical protein T19D2.1 - Caenorhabditis elegans

A;Map position: 1
A;Introns: 38/3; 92/3; 131/3; 169/1; 236/2; 282/3; 349/2; 376/2; 420/1; 576/3; 759/3; 84

Query Match 77.9%; Score 60; DB 2; Length 1059;
Best Local Similarity 66.7%; Pred. No. 0.87;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 29 WSPWSSCTKTCG 40

RESULT 8
TSHUP1
thrombospondin 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1987 #sequence revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A26155; A34274; A30140; A25812; A05172; A42927
R;Lawler, J.; Hynes, R.O.
J. Cell Biol. 103, 1635-1648, 1986
A;Title: The structure of human thrombospondin, an adhesive glycoprotein with multiple
A;Reference number: A26155; MUID:87057617; PMID:2430973
A;Accession: A26155
A;Molecule type: mRNA
A;Residues: 1-1170 <LAH>
A;Cross-references: UNIPROT:P07996; GB:X04665; NID:G371137; PIDN:CAA28370.1; PID:G371138
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
R;Laherty, C.D.; Gierman, T.M.; Dixit, V.M.
J. Biol. Chem. 264, 11222-11227, 1989
A;Title: Characterization of the promoter region of the human thrombospondin gene. DNA s
A;Reference number: A34274; MUID:89291870; PMID:2544587
A;Accession: A34274
A;Molecule type: DNA
A;Residues: 1-166 <LAH>
A;Cross-references: GB:J04835
R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotwein,
J. Cell Biol. 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites in th
A;Reference number: A30140; MUID:89139590; PMID:2918029
A;Accession: A30140
A;Molecule type: mRNA
A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>
A;Cross-references: EMBL:X14787; NID:G37464; PIDN:CAA32889.1; PID:G37465
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
A;Title: Partial amino acid sequence of human thrombospondin as determined by analysis o
A;Reference number: A25812; MUID:87157592; PMID:3030396
A;Accession: A25812
A;Molecule type: mRNA
A;Residues: 1-83,'A',85-397 <KOB>
A;Cross-references: GB:M25631; NID:G538353; PIDN:AAA36741.1; PID:G538354
R;Dixit, V.M.; Hennessy, S.W.; Grant, G.A.; Rotwein, P.; Frazier, W.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 5449-5453, 1986
A;Reference number: A05172; MUID:86287276; PMID:3461443
A;Accession: A05172
A;Molecule type: mRNA
A;Residues: 1-83,'A',85-374,'RC' <DIX>
A;Cross-references: GB:M14326; NID:G340005; PIDN:AAA61237.1; PID:G553801
A;Note: parts of this sequence, including the amino end of the mature protein, were deter
R;Sun, X.; Skorstengaard, K.; Mosher, D.F.
J. Cell Biol. 118, 693-701, 1992
A;Title: Disulfides modulate RGD-inhibitable cell adhesive activity of thrombospondin.
A;Reference number: A42927; MUID:92348511; PMID:1379247
A;Accession: A42927
A;Molecule type: protein
A;Residues: 987-1003 <SUN>
A;Note: Cys-992 is shown to have a free sulfhydryl
C;Genetics:
A;Gene: GDB:THBS1; TSP1; TSP
A;Cross-references: GDB:120438; OMIM:188060
A;Map position: 15q15-15q15
A;Introns: 23/1

A;Note: the list of introns may be incomplete
C;Complex: homotrimer, disulfide linked
C;Function:

A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>

F;551-586/Domain: EGF homology <EGF1>
F;650-689/Domain: EGF homology <EGF2>

F;926-928/Region: cell attachment (R-G-D) motif
F;171-232/Disulfide bonds: #status predicted

F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;270,274/Disulfide bonds: interchain #status predicted

F;610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;1051/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 77.9%; Score 60; DB 1; Length 1170;
Best Local Similarity 75.0%; Pred. No. 0.93;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

Db 385 WSEWTSCTSCG 396
|||:|||||

RESULT 9

A38152

F-spondin - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A38152

R;Klar, A.; Baldassare, M.; Jessell, T.M.

Cell 69, 95-110, 1992

A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secreted
A;Reference number: A38152; MUID:92208952; PMID:1555244

A;Accession: A38152

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-807 <KLA>

A;Cross-references: UNIPROT:P35446; GB:M88469; NID:G204176; PIDN:AAA41174.1; PID:G204177

A;Experimental source: embryo floor plate

A;Note: sequence extracted from NCBI backbone (NCBI:90877, NCBI:90878)

C;Superfamily: F-spondin; thrombospondin type 1 repeat homology

F;441-495/Domain: thrombospondin type 1 repeat homology <THR2>

F;500-555/Domain: thrombospondin type 1 repeat homology <THR3>

F;557-611/Domain: thrombospondin type 1 repeat homology <THR4>

F;613-666/Domain: thrombospondin type 1 repeat homology <THR1>

F;667-721/Domain: thrombospondin type 1 repeat homology <THR5>

F;753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 76.6%; Score 59; DB 2; Length 807;
Best Local Similarity 66.7%; Pred. No. 0.97;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

Db 674 WSGWSECNKSCG 685
|||:|||||

RESULT 10

T29247

hypothetical protein F09F9.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T29247

R;Minx, P.; Hawkins, J.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of C. elegans cosmid F09F9.

Fri Apr 1 15:03:06 2005

J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: B42587
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1152; P', 1154-1170 <LAH>
A;Cross-references: GB:M87276
A;Note: sequence extracted from NCBI backbone (NCBIP:81501)
R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A;Title: Expression and initial characterization of recombinant mouse thrombospondin 1 ar
A;Reference number: S68787; MUID:96234006; PMID:8654563
A;Accession: S68787
A;Molecule type: protein
A;Residues: 19-26, 'X', 28-37 <CHE>
C;Complex: homotrimer, disulfide linked
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
C;Keywords: calcium binding; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1170/Product: thrombospondin 1 #status predicted <MAT>
F;317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F;378-429/Domain: thrombospondin type 1 repeat homology <THR1>
F;434-490/Domain: thrombospondin type 1 repeat homology <THR2>
F;491-547/Domain: thrombospondin type 1 repeat homology <THR3>
F;551-586/Domain: EGF homology <EGF>
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.3%; Score 58; DB 2; Length 1170;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 441 WSPWSSCSVTGC 452

RESULT 13
TSHUP2
Thrombospondin 2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: poter
A;Reference number: A47379; MUID:94010892; PMID:8406456
A;Accession: A47379
A;Molecule type: mRNA
A;Residues: 1-1172 <LAB>
A;Cross-references: UNIPROT:P35442; GB:112350; NID:G307505; PIDN:AAA03703.1; PID:G307506
R;LaBell, T.L.; Milewicz, D.J.; Distche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression of
A;Reference number: A42173; MUID:92217961; PMID:1559694
A;Accession: A42173
A;Molecule type: mRNA
A;Residues: 560-1172 <LA2>
A;Cross-references: GB:M81339
A;Experimental source: fibroblast
A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C;Genetics:
A;Gene: GDB:THBS2; TSP2
A;Cross-references: GDB:128789; OMIM:188061
A;Map position: 6q27-6q27
C;Complex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1172/Product: thrombospondin 2 #status predicted <MAT>
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>

A;Reference number: Z20594
A;Accession: T29247
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-654 <MIN>
A;Cross-references: UNIPROT:Q19284; EMBL:U40958; PIDN:AAA81764.1; CESP:F09F9.4
C;Genetics:
A;Gene: CESP:F09F9.4
A;Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

Query Match 75.3%; Score 58; DB 2; Length 654;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 322 WSEWSACSETCG 333

RESULT 11
A47723
F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47723
R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A;Reference number: A47723; MUID:93376785; PMID:8367492
A;Accession: A47723
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-803 <RU1>
A;Cross-references: UNIPROT:P35447; GB:L09123; NID:G409244; PIDN:AAA19105.1; PID:G409245
C;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 75.3%; Score 58; DB 2; Length 803;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 670 WSYWSECKNSCG 681

RESULT 12
A40558
Thrombospondin 1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40558; A37905; B42587; S68787
R;Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
Genomics 11, 587-600, 1991
A;Title: Characterization of the murine thrombospondin gene.
A;Reference number: A40558; MUID:92128941; PMID:1774063
A;Accession: A40558
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1170 <LAW>
A;Cross-references: UNIPROT:P35441; GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M6245
; GB:M62464; GB:M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:G5118
R;Bornstein, P.; Alfi, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A;Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
A;Reference number: A37905; MUID:90375546; PMID:2398070
A;Accession: A37905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <BOR>
A;Cross-references: GB:J05605; GB:J05606; NID:G201991; PIDN:AAA40431.1; PID:G554390
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.

F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF1>
F;652-691/Domain: EGF homology <EGF>
F;928-930/Region: cell attachment (R-G-D) motif
F;151,316,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;167-226/Disulfide bonds: #status predicted
F;266,270/Disulfide bonds: interchain #status predicted
F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 75.3%; Score 58; DB 1; Length 1172;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||||| :||
Db 443 WSPWSSCSVTCTG 454

RESULT 14
A42587
thrombospondin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42587; A39851
R;LaHerty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: A42587
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-1172 <LAH>
A;Cross-references: UNIPROT:Q03350; GB:L07803; GB:M87275; NID:g340421; PIDN:AAA53064.1;
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
J. Biol. Chem. 266, 12821-12824, 1991
A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A;Reference number: A39851; MUID:91302287; PMID:1712771
A;Accession: A39851
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-873 <BOR>
A;Cross-references: GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:g201995
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
C;Keywords: calcium binding; glycoprotein
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF1>
F;652-691/Domain: EGF homology <EGF>

Query Match 75.3%; Score 58; DB 2; Length 1172;
Best Local Similarity 75.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
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Db 443 WSPWSSCSVTCTG 454

RESULT 15
A39804
thrombospondin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A39804
R;Lawler, J.; Duquette, M.; Ferro, P.
J. Biol. Chem. 266, 8039-8043, 1991
A;Title: Cloning and sequencing of chicken thrombospondin.
A;Reference number: A39804; MUID:91217026; PMID:2022631

A;Accession: A39804
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1178 <LAW>
A;Cross-references: UNIPROT:P35440; GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764
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F;325-383/Domain: von Willebrand factor type C repeat homology <VWC>
F;386-437/Domain: thrombospondin type 1 repeat homology <THR1>
F;442-498/Domain: thrombospondin type 1 repeat homology <THR2>
F;499-555/Domain: thrombospondin type 1 repeat homology <THR3>
F;658-697/Domain: EGF homology <EGF>

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Best Local Similarity 75.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
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Db 449 WSPWSSCSVTCTG 460

Search completed: April 1, 2005, 14:00:30
Job time : 16.6957 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:59:39 ; Search time 61.8261 Seconds
(without alignments)
64.360 Million cell updates/sec

Title: US-09-462-909D-8
Perfect score: 77
Sequence: 1 WSGWSSCSRSCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	68	88.3	4123	14 US-10-213-509-5	Sequence 5, Appli
2	68	88.3	4219	15 US-10-085-198-2	Sequence 2, Appli
3	65	84.4	997	9 US-09-918-171A-7	Sequence 7, Appli
4	65	84.4	997	10 US-09-981-151A-32	Sequence 32, Appl
5	65	84.4	997	16 US-10-408-765A-1094	Sequence 1094, Ap
6	65	84.4	1255	15 US-10-312-352-23	Sequence 23, Appl
7	65	84.4	1686	15 US-10-386-414-2	Sequence 2, Appli
8	65	84.4	1690	9 US-09-788-043C-5	Sequence 5, Appli
9	64	83.1	353	15 US-10-161-493-132	Sequence 132, App
10	63	81.8	415	10 US-09-800-198-89	Sequence 89, Appl
11	63	81.8	571	15 US-10-262-839-180	Sequence 180, App
12	63	81.8	577	15 US-10-262-839-196	Sequence 196, App
13	63	81.8	791	10 US-09-981-151A-4	Sequence 4, Appli

14	63	81.8	856	10 US-09-981-151A-6	Sequence 6, Appli
15	63	81.8	952	10 US-09-981-151A-8	Sequence 8, Appli
16	63	81.8	986	10 US-09-981-151A-2	Sequence 2, Appli
17	63	81.8	1224	13 US-10-217-774-4	Sequence 4, Appli
18	63	81.8	1224	14 US-10-296-616-2	Sequence 2, Appli
19	63	81.8	1224	15 US-10-275-107-51	Sequence 51, Appl
20	63	81.8	1224	17 US-10-804-457-4	Sequence 4, Appli
21	63	81.8	1236	15 US-10-399-645-4	Sequence 4, Appli
22	63	81.8	1365	15 US-10-120-801-48	Sequence 48, Appl
23	63	81.8	1490	15 US-10-262-839-184	Sequence 184, App
24	63	81.8	1545	15 US-10-262-839-182	Sequence 182, App
25	63	81.8	1549	15 US-10-262-839-186	Sequence 186, App
26	63	81.8	1588	13 US-10-000-512-2	Sequence 2, Appli
27	63	81.8	1588	15 US-10-074-566-2	Sequence 2, Appli
28	63	81.8	1588	15 US-10-074-566-41	Sequence 41, Appl
29	63	81.8	1588	15 US-10-262-839-176	Sequence 176, App
30	63	81.8	1588	15 US-10-262-839-188	Sequence 188, App
31	63	81.8	1588	15 US-10-262-839-194	Sequence 194, App
32	63	81.8	1588	15 US-10-262-839-200	Sequence 200, App
33	63	81.8	1624	17 US-10-363-374-6	Sequence 6, Appli
34	62	80.5	349	15 US-10-161-493-126	Sequence 126, App
35	62	80.5	353	15 US-10-161-493-128	Sequence 128, App
36	62	80.5	353	15 US-10-161-493-130	Sequence 130, App
37	62	80.5	353	15 US-10-161-493-134	Sequence 134, App
38	62	80.5	661	15 US-10-354-983-8	Sequence 8, Appli
39	62	80.5	862	14 US-10-226-560-2	Sequence 2, Appli
40	62	80.5	914	15 US-10-188-186-132	Sequence 132, App
41	62	80.5	919	15 US-10-188-186-130	Sequence 130, App
42	62	80.5	934	15 US-10-275-107-53	Sequence 53, Appl
43	62	80.5	1071	15 US-10-354-983-4	Sequence 4, Appli
44	62	80.5	1081	15 US-10-120-801-46	Sequence 46, Appl
45	62	80.5	1081	16 US-10-391-364-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-10-213-509-5
; Sequence 5, Application US/10213509
; Publication No. US20030054485A1
; GENERAL INFORMATION:
; APPLICANT: Weibs, Joseph
; APPLICANT: Scott, Matthew
; TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
; FILE REFERENCE: STAN-232
; CURRENT APPLICATION NUMBER: US/10/213,509
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/311,720
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4123
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-213-509-5

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Db 2518 WSVWSSCSRSCG 2529

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US-10-085-198-2
; Sequence 2, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
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; LENGTH: 4219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-2

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QY 1 WSGWSSCSRSCG 12
DB 2614 WSWSSCSRSCG 2625

RESULT 3
US-09-918-171A-7
; Sequence 7, Application US/09918171A
; Patent No. US20020110894A1
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/04193
; CURRENT APPLICATION NUMBER: US/09/918,171A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/369,364
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-7
US-09-918-171A-7

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DB 544 WSAWSICSRSCG 555

RESULT 4
US-09-981-151A-32
; Sequence 32, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glennnda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shinkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
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; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
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; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
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; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-32

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Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
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RESULT 5
US-10-408-765A-1094
; Sequence 1094, Application US/10408765A
; Publication No. US20040101874A1

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; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 66088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1094
; LENGTH: 997
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; ORGANISM: Homo sapiens
US-10-408-765A-1094
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; Publication No. US20040053824A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: HE, Ann; BATRA, Sajeev
; APPLICANT: LO, Terence P.; NGUYEN, Danniell B.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam
; APPLICANT: BURFORD, Neil; YAO, Monique G.
; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
; APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
; APPLICANT: LU, Yan; BOROWSKY, Mark L.
; APPLICANT: LU, Dyung Aina M.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
; APPLICANT: XU, Yuming; KALLICK, Deborah A.
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
; APPLICANT: DELEGEANE, Angelo M.; LEE, Sally
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PF-0794 USN
; CURRENT APPLICATION NUMBER: US/10/312,352
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/US01/21067
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,454
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/219,462
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 60/240,111
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/240,106
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/244,021
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/248,887
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/249,570
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; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 23
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053824A1 55022490CD1
US-10-312-352-23
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Best Local Similarity 83.3%; Pred. No. 4.5;
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Db      113 WSAWSICSRSCG 124
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RESULT 7

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; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0210MNM
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
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; LENGTH: 1686
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-386-414-2
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Best Local Similarity 83.3%; Pred. No. 5.6;
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us-09-462-909d-8.rapb

Fri Apr 1 15:03:05 2005

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; FILE REFERENCE: 21402-377A
; CURRENT APPLICATION NUMBER: US/10/161,493
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/337,524
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,575
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/359,151
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,573
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/341,143
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 299
; SEQ ID NO 132
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-161-493-132

Query Match      83.1%; Score 64; DB 15; Length 353;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 WSGWSSCSRSCG 12
      |||||
Db      303 WSNWSECSRTC 314

RESULT 10
US-09-800-198-89
; Sequence 89, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Halocynthia roretzi
; US-09-800-198-89

Query Match      81.8%; Score 63; DB 10; Length 415;
Best Local Similarity 75.0%; Pred. No. 3.3;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 WSGWSSCSRSCG 12
      |||||
; US-10-161-493-132
; Sequence 132, Application US/10161493
; Publication No. US20040018555A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A
; APPLICANT: Gorman, Linda
; APPLICANT: Pena, Carol EA
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leite, Mario W
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Miller, Charles E
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Hjal, Tord
; APPLICANT: Voss, Edward Z
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Ji, Weizhen
; APPLICANT: Smithson, Glennda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; TITLE OF INVENTION: No. US20040018555A1el Antibodies that Bind to Antigenic Polypepti
; TITLE OF INVENTION: Acids Encoding the Antigens, and Methods of Use
; US-09-788-043C-5
; Sequence 5, Application US/09788043C
; Patent No. US20020107361A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Renu
; APPLICANT: Zuo, Fengrong
; APPLICANT: Klonowski, Paul
; TITLE OF INVENTION: No. US20020107361A1el Metalloproteases Having
; TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: ROCH-004
; CURRENT APPLICATION NUMBER: US/09/788,043C
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/184,152
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1690
; TYPE: PRT
; ORGANISM: human
; US-09-788-043C-5

Query Match      84.4%; Score 65; DB 9; Length 1690;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 WSGWSSCSRSCG 12
      |||||
Db      548 WSAWSICSRSCG 559

RESULT 9
US-10-161-493-132
; Sequence 132, Application US/10161493
; Publication No. US20040018555A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A
; APPLICANT: Gorman, Linda
; APPLICANT: Pena, Carol EA
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leite, Mario W
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Miller, Charles E
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Hjal, Tord
; APPLICANT: Voss, Edward Z
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Ji, Weizhen
; APPLICANT: Smithson, Glennda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; TITLE OF INVENTION: No. US20040018555A1el Antibodies that Bind to Antigenic Polypepti
; TITLE OF INVENTION: Acids Encoding the Antigens, and Methods of Use
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Db 320 WTTWSSCSKSCG 331

RESULT 11

US-10-262-839-180
; Sequence 180, Application US/10262839
; Publication No. US20040038877A1
; GENERAL INFORMATION:

; APPLICANT: Alsobrook, John,
; APPLICANT: Anderson, David W.,
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Catterton, Elina,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Leach, Martin,
; APPLICANT: Li, Li,
; APPLICANT: Miller, Charles,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Shinkets, Richard,
; APPLICANT: Smithson, Glennnda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Voss, Edward,
; APPLICANT: Zerhusen, Brian,
; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-462A

; CURRENT APPLICATION NUMBER: US/10/262,839

; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: 60/326,483

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: 60/327,917

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,029

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,056

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/381,101

; PRIOR FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 60/371,972

; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: 60/327,342

; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/328,044

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/374,738

; PRIOR FILING DATE: 2002-04-23

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 367

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 180

; LENGTH: 571

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-262-839-180

Query Match 81.8%; Score 63; DB 15; Length 571;

Best Local Similarity 75.0%; Pred. No. 4.3;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

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Db 124 WSNWRCCKSCG 135

RESULT 12

US-10-262-839-196
; Sequence 196, Application US/10262839
; Publication No. US20040038877A1
; GENERAL INFORMATION:

; APPLICANT: Alsobrook, John,
; APPLICANT: Anderson, David W.,
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Catterton, Elina,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Leach, Martin,
; APPLICANT: Li, Li,
; APPLICANT: Miller, Charles,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Shinkets, Richard,
; APPLICANT: Smithson, Glennnda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Voss, Edward,
; APPLICANT: Zerhusen, Brian,
; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-462A

; CURRENT APPLICATION NUMBER: US/10/262,839

; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: 60/326,483

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: 60/327,917

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,029

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,056

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/381,101

; PRIOR FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 60/371,972

; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: 60/327,342

; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/328,044

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/328,849

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/374,738

; PRIOR FILING DATE: 2002-04-23

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 367

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 196

; LENGTH: 577

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-262-839-196

Query Match 81.8%; Score 63; DB 15; Length 577;

Best Local Similarity 75.0%; Pred. No. 4.3;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

|| || || || ||

Db 125 WSNWSCSKSCG 136

RESULT 13

US-09-981-151A-4
; Sequence 4, Application US/09981151A
; Publication No. US20030212256A1

GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-168

; CURRENT APPLICATION NUMBER: US/09/981,151A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 60/241,040

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,058

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,063

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,243

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/242,152

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/242,482

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,611

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,612

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,880

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 60/242,881

; PRIOR FILING DATE: 2000-10-24

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 791

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-981-151A-4

Query Match 81.8%; Score 63; DB 10; Length 791;

Best Local Similarity 75.0%; Pred. No. 5.5;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

||| ||| ||| |||

Db 477 WSSWSPCSRSCG 488

RESULT 14

US-09-981-151A-6
; Sequence 6, Application US/09981151A
; Publication No. US20030212256A1

GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-168

; CURRENT APPLICATION NUMBER: US/09/981,151A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 60/241,040

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,058

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,063

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/241,243

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/242,152

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/242,482

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,611

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,612

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/242,880

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 60/242,881

; PRIOR FILING DATE: 2000-10-24

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 856

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-981-151A-6

Query Match 81.8%; Score 63; DB 10; Length 856;

Best Local Similarity 75.0%; Pred. No. 5.9;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

||| ||| ||| |||

Db 543 WSSWSPCSRSCG 554

RESULT 15

US-09-981-151A-8

; Sequence 8, Application US/09981151A

; Publication No. US20030212256A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 952
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-8

Query Match 81.8%; Score 63; DB 10; Length 952;
Best Local Similarity 75.0%; Pred. No. 6.4;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| |||:
Db 629 WSSWSPCSRTOG 640

Search completed: April 1, 2005, 14:22:17
Job time : 61.8261 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:44:22 ; Search time 21.1304 Seconds
(without alignments)
42.393 Million cell updates/sec

Title: US-09-462-909D-8
Perfect score: 77
Sequence: 1 WSGWSSCSRSCG 12

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	84.4	997	3	US-09-369-364A-7
2	63	81.8	1224	4	US-09-930-872-4
3	63	81.8	1224	4	US-10-217-774-4
4	60	77.9	23	1	US-07-646-531D-5
5	60	77.9	23	2	US-08-488-273-5
6	60	77.9	23	3	US-09-197-770B-11
7	60	77.9	23	6	5426100-5
8	60	77.9	23	6	5426100-5
9	60	77.9	218	3	US-08-985-526-1
10	60	77.9	239	5	PCT-US93-01652-1
11	60	77.9	441	3	US-08-985-526-3
12	60	77.9	1059	4	US-09-800-729-217
13	60	77.9	1170	1	US-08-313-288B-20
14	60	77.9	1170	4	US-09-657-472-2
15	59	76.6	52	2	US-08-799-173A-12
16	59	76.6	52	4	US-09-170-042A-12
17	59	76.6	56	1	US-07-862-021B-19
18	59	76.6	56	5	PCT-US93-03164-19
19	59	76.6	446	4	US-09-784-358-4
20	59	76.6	518	3	US-09-369-364A-22
21	59	76.6	724	4	US-09-784-358-8
22	59	76.6	787	4	US-09-825-294-207
23	59	76.6	787	4	US-09-970-966-207
24	59	76.6	807	1	US-07-862-021B-10
25	59	76.6	807	1	US-08-313-288B-10
26	59	76.6	807	4	US-09-132-769-1
27	59	76.6	807	4	US-09-132-769-3

28	59	76.6	807	4	US-09-132-769-5	Sequence 5, Appli
29	59	76.6	807	4	US-09-640-173-186	Sequence 186, App
30	59	76.6	807	4	US-09-713-550-186	Sequence 186, App
31	59	76.6	807	4	US-09-825-294-186	Sequence 186, App
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33	59	76.6	807	5	PCT-US93-03164-10	Sequence 10, Appl
34	59	76.6	845	4	US-09-784-358-12	Sequence 12, Appl
35	59	76.6	930	4	US-09-122-126B-15	Sequence 15, Appl
36	59	76.6	930	4	US-09-634-286A-15	Sequence 15, Appl
37	59	76.6	930	4	US-10-247-685-15	Sequence 15, Appl
38	59	76.6	1691	4	US-09-784-358-2	Sequence 2, Appli
39	58	75.3	23	1	US-07-646-531D-6	Sequence 6, Appli
40	58	75.3	23	2	US-08-488-273-6	Sequence 6, Appli
41	58	75.3	23	3	US-09-197-770B-12	Sequence 12, Appl
42	58	75.3	23	6	5426100-6	Patent No. 5426100
43	58	75.3	23	6	5426100-6	Patent No. 5426100
44	58	75.3	50	4	US-09-800-729-161	Sequence 161, App
45	58	75.3	60	1	US-07-646-531D-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-369-364A-7
; Sequence 7, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-7
US-09-369-364A-7

Query Match 84.4%; Score 65; DB 3; Length 997;
Best Local Similarity 83.3%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
Db 544 WSAWSICSRSCG 555

RESULT 2
US-09-930-872-4
; Sequence 4, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the San
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/09/930,872
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-930-872-4

Query Match 81.8%; Score 63; DB 4; Length 1224;
Best Local Similarity 75.0%; Pred. No. 4.9;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
Db 592 WSSWSPCSRTCG 603
RESULT 3
US-10-217-774-4
; Sequence 4, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-217-774-4

Query Match 81.8%; Score 63; DB 4; Length 1224;
Best Local Similarity 75.0%; Pred. No. 4.9;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
Db 592 WSSWSPCSRTCG 603

RESULT 4
US-07-646-531D-5
; Sequence 5, Application US/07646531D
; Patent No. 5200397
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan Howard
; APPLICANT: Tuszyński, George Paul
; TITLE OF INVENTION: Peptide Fragments and Analogs of
; TITLE OF INVENTION: Thrombospondin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. R. Grace & Co.-Conn.
; STREET: 7379 Route 32
; CITY: Columbia
; STATE: Maryland
; COUNTRY: USA
; ZIP: 21044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,531D
; FILING DATE: 19910131
; ATTORNEY/AGENT INFORMATION:
; NAME: Appleby, Vanessa L.
; REGISTRATION NUMBER: 33223
; REFERENCE/DOCKET NUMBER: 01-7896
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 531-4515

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-646-531D-5
Query Match 77.9%; Score 60; DB 1; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
Db 4 WSEWTSCSTSCG 15
RESULT 5
US-08-488-273-5
; Sequence 5, Application US/08488273
; Patent No. 5840692
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan H.
; APPLICANT: Tuszyński, George P.
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; TITLE OF INVENTION: THROMBOSPONDIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,273
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/359,263
; FILING DATE: 19-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,527
; FILING DATE: 09-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/483,527
; FILING DATE: 22-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-2U4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-273-5

Query Match 77.9%; Score 60; DB 2; Length 23;

Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 4 WSEWTSCSTSCG 15

RESULT 6

US-09-197-770B-11
; Sequence 11, Application US/09197770B
; Patent No. 6339062
; GENERAL INFORMATION:
; APPLICANT: Tuszyński, George
; APPLICANT: Williams, Taffy
; APPLICANT: Actor, Paul
; TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
; TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
; FILE REFERENCE: 07206-0021
; CURRENT APPLICATION NUMBER: US/09/197,770B
; CURRENT FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770B-11

Query Match 77.9%; Score 60; DB 3; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 4 WSEWTSCSTSCG 15

RESULT 7

5426100-5
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO:5:
; LENGTH: 23
5426100-5

Query Match 77.9%; Score 60; DB 6; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 4 WSEWTSCSTSCG 15

RESULT 8

5426100-5
; Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE

; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
; SEQ ID NO:5:
; LENGTH: 23
5426100-5

Query Match 77.9%; Score 60; DB 6; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.39;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||:|||||
Db 4 WSEWTSCSTSCG 15

RESULT 9

US-08-985-526-1
; Sequence 1, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19899
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,526
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,845
; FILING DATE: 16-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: McMorow Jr., Robert G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 658-9141
; TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-985-526-1

Query Match 77.9%; Score 60; DB 3; Length 218;
Best Local Similarity 75.0%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
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Db 85 WSEWTSCSTSCG 96

us-09-462-909d-8.ra1

Fri Apr 1 15:03:05 2005

STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: McMorow Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-985-526-3

Query Match 77.9%; Score 60; DB 3; Length 441;
Best Local Similarity 75.0%; Pred. No. 4.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
Db 85 WSEWTSCTSCG 96

RESULT 12
US-09-800-729-217
; Sequence 217, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-217

Query Match 77.9%; Score 60; DB 4; Length 1059;
Best Local Similarity 66.7%; Pred. No. 9.9;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
Db 29 WSPWSSCTKTCG 40

RESULT 13
US-08-313-288B-20
; Sequence 20, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar

RESULT 10
PCT-US93-01652-1
; Sequence 1, Application PC/TUS9301652
; GENERAL INFORMATION:
; APPLICANT: Bouck, Noel P.
; APPLICANT: Polverini, Peter J.
; APPLICANT: Good, Deborah J.
; APPLICANT: Frazier, William A.
; TITLE OF INVENTION: Method and Composition for
; TITLE OF INVENTION: Inhibiting Angiogenesis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive, Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01652
FILING DATE: 19930222
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/841,656
FILING DATE: 24-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/464,369
FILING DATE: 12-JAN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rentress, Susan B.
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: 92005-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000
TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US93-01652-1

Query Match 77.9%; Score 60; DB 5; Length 239;
Best Local Similarity 75.0%; Pred. No. 2.8;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
Db 74 WSEWTSCTSCG 85

RESULT 11
US-08-985-526-3
; Sequence 3, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A
; TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
; TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Connolly, Bove, Lodge, & Hutz
; STREET: 1220 Market Street, P.O. Box 2207
; CITY: Wilmington

```

; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
;
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
;
; NUMBER OF SEQUENCES: 20
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Cooper & Dunham LLP
;
; STREET: 1185 Avenue of the Americas
;
; CITY: New York
;
; STATE: New York
;
; COUNTRY: USA
;
; ZIP: 10036
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/313,288B
;
; FILING DATE: January 5, 1995
;
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: White, John P.
;
; REGISTRATION NUMBER: 28,678
;
; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (212) 278-0400
;
; TELEFAX: (212) 391-0526
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 20:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1170 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: single
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; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
;
; US-08-313-288B-20

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Query Match 77.9%; Score 60; DB 1; Length 1170;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 385 WSEWTSCTSTSCG 396

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RESULT 14
US-09-657-472-2
; Sequence 2, Application US/09657472
; Patent NO. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-657-472-2

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Query Match	77.9%;	Score 60;	DB 4;	Length 1170;
Best Local Similarity	75.0%;	Pred. No. 11;		
Matches 9;	Conservative	1;	Mismatches	2; Indels 0; Gaps 0;

Qy 1 WSGWSSCSRSCG 12
Db 385 WSEWTSCTSCG 396

RESULT 15
US-08-799-173A-12
; Sequence 12, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG,
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,173A
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-799-173A-12

Query Match	76.6%	Score 59;	DB 2;	Length 52;
Best Local Similarity	66.7%	Pred. No. 1;		
Matches	8;	Conservative	2;	Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
Db 6 WSQWSECNKSCG 17

Search completed: April 1, 2005, 14:01:57
Job time : 21.1304 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:22:55 ; Search time 83.7391 Seconds
(without alignments)
55.424 Million cell updates/sec

Title: US-09-462-909D-8
Perfect score: 77
Sequence: 1 WSGWSSCSRSCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	68	88.3	606	ADP04709	Adp04709 Sea squir
3	68	88.3	4123	ABU62079	Abu62079 Human jel
4	68	88.3	4219	ADH48718	Adh48718 NOV1 prot
5	68	88.3	4561	ABG30203	Abg30203 Novel hum
6	68	88.3	5737	ADN95228	Adn95228 Human BEC
7	68	88.3	9222	ABG21064	Abg21064 Novel hum
8	65	84.4	997	AAB72283	Aab72283 Human ADA
9	65	84.4	997	ADJ69288	Adj69288 Human hea
10	65	84.4	1054	ABB60410	Abb60410 Drosophil
11	65	84.4	1255	ADI28031	Adi28031 ECMCAD pr
12	65	84.4	1686	AAE00934	Aae00934 Human 278
13	65	84.4	1686	AAE00913	Aae00913 Human 278
14	65	84.4	1686	AAB74944	Aab74944 Human ADA
15	65	84.4	1686	ADJ58902	Adj58902 Human ADA
16	65	84.4	1690	AAB86949	Aab86949 Human met
17	65	84.4	1784	AAB41379	Aab41379 Human ORF
18	64	83.1	353	ABJ19383	Abj19383 NOVX rela
19	64	83.1	353	ADO41766	Ado41766 Novel hum
20	63	81.8	556	ABG31503	Abg31503 Human ADA
21	63	81.8	571	ABR58452	Abr58452 Human NOV
22	63	81.8	577	ABR58460	Abr58460 Human NOV
23	63	81.8	722	ADA50469	Ada50469 Human pro
24	63	81.8	791	ABG76895	Abg76895 Human zin
25	63	81.8	791	ADJ38422	Adj38422 Human nov

26	63	81.8	856	5	ABG76896	Abg76896 Human ADA
27	63	81.8	856	7	ADJ38424	Adj38424 Human nov
28	63	81.8	928	8	ADR09503	Adr09503 Human pro
29	63	81.8	952	5	ABG76897	Abg76897 Human ADA
30	63	81.8	952	7	ADJ38426	Adj38426 Human nov
31	63	81.8	986	5	ABG76894	Abg76894 Human zin
32	63	81.8	986	7	ADJ38420	Adj38420 Human nov
33	63	81.8	1021	5	AAU79496	Aau79496 Human par
34	63	81.8	1072	6	ABR40093	Abr40093 Human ADA
35	63	81.8	1170	5	AAU79500	Aau79500 Human ADA
36	63	81.8	1224	5	AAU72891	Aau72891 Human met
37	63	81.8	1224	5	AAO15254	Aao15254 Human MDT
38	63	81.8	1224	5	AAU79497	Aau79497 Human ADA
39	63	81.8	1224	5	AAU80153	Aau80153 Human ADA
40	63	81.8	1224	6	ABG72431	Abg72431 Novel hum
41	63	81.8	1224	6	ABR83432	Abr83432 Human ADA
42	63	81.8	1224	7	ADA50762	Ada50762 Novel hum
43	63	81.8	1224	8	ABM79745	Abm79745 Human pro
44	63	81.8	1236	5	AAU98886	Aau98886 Human pro
45	63	81.8	1237	8	ABM84501	Abm84501 Human dia

ALIGNMENTS

RESULT 1
AAW97445
ID AAW97445 standard; peptide; 12 AA.
XX
AC AAW97445;
XX
DT 19-MAY-1999 (first entry)
XX
DE Peptide that is useful for regenerating the nervous system.
XX
KW Neuronal sprouting; cerebral cortex; spinal cord cell; aggregation;
KW neurite defasciculation; regeneration; nervous system cell;
KW neurodegeneration; Alzheimer's; Parkinson's disease; multiple sclerosis;
KW myopathy; synapse formation; neuroblastoma.
XX
OS Synthetic.
XX
PN WO9903890-A1.
XX
PD 28-JAN-1999.
XX
PF 16-JUL-1998; 98WO-FR001556.
XX
PR 16-JUL-1997; 97FR-00009016.
XX
PA (UYAU-) UNIV AUVERGNE.
XX
PI Meinier A, Monnerie H, Gobron S;
XX
DR WPI; 1999-132166/11.
XX
PT New polypeptides for promoting growth of neurons - useful for treatment of neurodegeneration, neuroblastoma and as additives for neuronal cell cultures.
XX
PS Claim 6; Page 14; 29pp; French.
XX
CC The present sequence represents a peptide that stimulates neuronal (particularly axonal) sprouting in neurons of the cerebral cortex, and in spinal cord cells inhibits aggregation and defasciculation of neurites while increasing formation of synaptic contacts. The peptide is used to regenerate nervous system cells, particularly for treating neurodegeneration (e.g. Alzheimer's or Parkinson's diseases, multiple sclerosis and myopathy), other conditions requiring regeneration (particularly elongation and synapse formation) or neuroblastoma. The peptide can also be used as an additive for neuronal cell cultures
XX
SQ Sequence 12 AA;

Fri Apr 1 15:03:05 2005

Query Match

Best Local Similarity

Matches 12; Conservative

100.0%; Score 77; DB 2; Length 12;

100.0%; Pred. No. 0.0019;

0; Mismatches 0; Indels 0; Gaps 0;

QY

1 WSGWSSCSRSCG 12

|||||

Db

1 WSGWSSCSRSCG 12

|||||

RESULT 2

ADP04709

ID ADP04709 standard; protein; 606 AA.

XX AC ADP04709;

XX DT 29-JUL-2004 (first entry)

XX DE Sea squirt protein with tissue specific expression in development Seq304.

XX KW sea squirt; regeneration medicine; gene therapy; cell proliferation;

XX KW differentiation; reproduction; environmental measurement; water survey.

XX OS Ciona intestinalis.

XX PN JP2004057129-A.

XX PD 26-FEB-2004.

XX PF 31-JUL-2002; 2002JP-00222593.

XX PR 31-JUL-2002; 2002JP-00222593.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX DR WPI; 2004-287079/27.

XX DR N-PSDB; ADP04708.

XX PT Novel gene cluster which is specifically expressed in tissue or organ

XX PT during developmental phase of sea squirt, useful for elucidation of

XX PT mechanism of development of tissue or organ of sea squirt.

XX PS Claim 1; SEQ ID NO 304; 1846pp; Japanese.

XX CC This invention relates to novel genes and the encoded proteins thereof

XX CC that are derived from the sea squirt Ciona intestinalis. Specifically, it

XX CC refers to those genes that are expressed in the tissues or organs of the

XX CC sea squirt during its developmental phase. The present invention

XX CC describes the identification of these genes as useful for elucidation of

XX CC the mechanism of development and hence for developing regeneration

XX CC medicines and gene therapy techniques. Accordingly, they can be used in

XX CC the research of various genetic diseases, as well as the analysis of cell

XX CC proliferations can be useful for environmental measurements and water

XX CC compositions, differentiation and reproduction. Furthermore, such

XX CC surveys, particularly for sea water surveys, and also for the preparation

XX CC of transformed sea squirt for improving edibility of sea squirt such as

XX CC Halocynthia roretzi. This polypeptide sequence is a sea squirt protein

XX CC sequence that has tissue specific expression during development, given in

XX CC an exemplification of the invention.

XX SQ Sequence 606 AA;

Query Match

Best Local Similarity

Matches 10; Conservative

88.3%; Score 68; DB 8; Length 606;

83.3%; Pred. No. 0.85;

1; Mismatches 1; Indels 1; Gaps 0;

QY

1 WSGWSSCSRSCG 12

|||||

Db

257 WTGWSSCSASCG 268

|||||

RESULT 3

ABU62079

ID ADH48718 standard; protein; 4219 AA.

XX AC ADH48718;

XX DT 25-MAR-2004 (first entry)

XX DE NOV1 protein sequence, SEQ ID 2.

XX KW Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic;

XX KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV1;

XX KW DJ0751H13.1 protein-like protein; chromosome 8.

XX OS Homo sapiens.

XX PN WO200268652-A2.

ID

XX

AC

XX

DT

XX

DE

XX

KW

KW

KW

KW

XX

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PA

XX

PI

XX

DR

XX

PT

XX

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

ABU62079 standard; protein; 4123 AA.

ABU62079;

16-SEP-2003 (first entry)

Human jelly belly (jeb) protein.

Human; jelly belly protein; jeb; visceral mesoderm migration;

differentiation; neuron; late embryogenesis; LDL receptor repeat;

development of nervous system; low density lipoprotein receptor;

hyperproliferative disorder; atherosclerosis; antiarteriosclerotic.

Homo sapiens.

US2003054485-A1.

20-MAR-2003.

06-AUG-2002; 2002US-00213509.

09-AUG-2001; 2001US-0311720P.

(SCOT/) SCOTT M P.

(WEIS/) WEISS J B.

Scott MP, Weiss JB;

WPI; 2003-540614/51.

New jelly belly gene, useful for preparing a composition for treating

hyperproliferative disorders e.g., atherosclerosis.

Disclosure; Page 18-28; 40pp; English.

The present invention relates to the isolation of fruitfly (Drosophila

melanogaster) jelly belly (jeb) protein, and the polynucleotide sequence

encoding it. Jeb is required for visceral mesoderm migration and

differentiation. Jeb is expressed in neurons in late embryogenesis

indicating that it may play a role in the development of the nervous

system. The jeb protein contains a LDL (low density lipoprotein) receptor

repeat. The polynucleotide sequence encoding jeb is useful for preparing

a composition for treating hyperproliferative disorders such as

atherosclerosis. The present sequence represents human jeb protein

Sequence 4123 AA;

Query Match

Best Local Similarity

Matches 11; Conservative

88.3%; Score 68; DB 7; Length 4123;

91.7%; Pred. No. 4.5;

0; Mismatches 1; Indels 0; Gaps 0;

QY

1 WSGWSSCSRSCG 12

|||||

Db

2518 WSVWSSCSRSCG 2529

|||||

RESULT 4

ADH48718

ID ADH48718 standard; protein; 4219 AA.

XX AC ADH48718;

XX DT 25-MAR-2004 (first entry)

XX DE NOV1 protein sequence, SEQ ID 2.

XX KW Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic;

XX KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV1;

XX KW DJ0751H13.1 protein-like protein; chromosome 8.

XX OS Homo sapiens.

XX PN WO200268652-A2.

XX 06-SEP-2002.
XX
XX
XX 26-FEB-2002; 2002WO-US005910.
XX
XX 26-FEB-2001; 2001US-0271646P.
PR 27-FEB-2001; 2001US-0271840P.
PR 28-FEB-2001; 2001US-0272404P.
PR 28-FEB-2001; 2001US-0272405P.
PR 28-FEB-2001; 2001US-0272410P.
PR 28-FEB-2001; 2001US-0272414P.
PR 02-MAR-2001; 2001US-0272787P.
PR 02-MAR-2001; 2001US-0272922P.
PR 02-MAR-2001; 2001US-0273048P.
PR 02-MAR-2001; 2001US-0273300P.
PR 16-MAR-2001; 2001US-0276401P.
PR 20-MAR-2001; 2001US-0277324P.
PR 20-MAR-2001; 2001US-0278660P.
PR 30-MAR-2001; 2001US-0280039P.
PR 30-MAR-2001; 2001US-0280234P.
PR 02-APR-2001; 2001US-0280818P.
PR 12-APR-2001; 2001US-0283443P.
PR 23-APR-2001; 2001US-0285754P.
PR 24-APR-2001; 2001US-0286096P.
PR 03-MAY-2001; 2001US-0288353P.
PR 17-MAY-2001; 2001US-0291703P.
PR 31-MAY-2001; 2001US-0294834P.
PR 20-JUN-2001; 2001US-0299695P.
PR 21-JUN-2001; 2001US-0299845P.
PR 05-JUL-2001; 2001US-0303242P.
PR 13-AUG-2001; 2001US-0311981P.
PR 16-AUG-2001; 2001US-0312858P.
PR 17-AUG-2001; 2001US-0313280P.
PR 29-AUG-2001; 2001US-0315614P.
PR 17-SEP-2001; 2001US-0322818P.
PR 25-FEB-2002; 2002US-00322818.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE;
PI Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA;
PI Gorman L, Guo X, Gusev VY, Kekuda R, Li L, Liu X, Malyankar UM;
PI Miller CE, Millet I, Padigar M, Patturajan M, Pena CEA, Peyman JA;
PI Rastelli L, Shenoy SG, Shimkets RA, Smithson G, Spytek KA, Stone DJ;
PI Taupier RJ, Tchernev VT, Vernet CAM, Zerhusen BD;
XX
XX WPI; 2002-698672/75.
DR N-PSDB; ADH48717.
XX
XX New NOVX polypeptides or polynucleotides, useful for preventing or
PT treating disorders or syndromes e.g., atherosclerosis, hypertension,
PT obesity or cancer.
XX
XX Claim 1; Page 13-14; 923pp; English.
XX
XX The present invention relates to novel human NOVX proteins, where X is
CC any number from 1 to 91 and their coding sequences. The proteins and
CC coding sequences are useful for preventing or treating disorders or
CC syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV1 is
CC a DJ0751H13.1 protein-like protein and its coding sequence maps to
CC chromosome 8.
XX
XX Sequence 4219 AA;
SQ

Query Match 88.3%; Score 68; DB 5; Length 4219;
Best Local Similarity 91.7%; Pred. No. 4.6;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
Db 2614 WSVWSSCSRSCG 2625

RESULT 5
ABG30203
ID ABG30203 standard; protein; 4561 AA.
XX
XX AC ABG30203;
XX
XX 18-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #30194.
XX
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO200175067-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US008631.
XX
XX PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS94390.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 60562; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 4561 AA;
SQ

Query Match 88.3%; Score 68; DB 4; Length 4561;
Best Local Similarity 91.7%; Pred. No. 5;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
Db 1481 WSVWSSCSRSCG 1492

RESULT 6
ADN95228

Fri Apr 1 15:03:05 2005

ID ADN95228 standard; protein; 5737 AA.
XX
AC ADN95228;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human BEC/LEC-related protein sequence SeqID150.
XX
KW growth; differentiation; blood endothelial cell; BEC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
KW inflammatory disease; cancer metastasis; lymphatic system; human.
XX
OS Homo sapiens.
XX
PN WO2003080640-A1.
XX
PD 02-OCT-2003.
XX
PF 07-MAR-2003; 2003WO-US006900.
XX
PR 07-MAR-2002; 2002US-0363019P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX
DR WPI; 2003-876899/81.
DR N-PSDB; ADN95229.
XX
PS Example 1; SEQ ID NO 150; 176pp; English.
XX
CC This invention relates to a method of differentially modulating the
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC endothelial cells (LEC) comprising contacting endothelial cells with a
CC composition comprising an agent that differentially modulates blood or
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC identifying a human subject with lymphoedema and with a mutation in at
CC least one allele of a gene encoding a LEC protein, where the mutation
CC correlates with lymphoedema in human subjects, and with the proviso that
CC the LEC protein is not VEGFR-3; and administering to the subject a
CC composition comprising a lymphatic growth agent selected from VEGF-C or
CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
CC the development of compounds with an antiangiogenic, cytostatic,
CC vasotropic or antiinflammatory activity or for gene therapy. The method
CC is useful in modulating the growth or differentiation of blood
CC endothelial cells or lymphatic endothelial cells, in treating hereditary
CC lymphoedema, in screening for an endothelial cell disorder or
CC predisposition to the disorder or in monitoring the efficacy or toxicity
CC of a drug on endothelial cells. The agent is useful in manufacturing a
CC medicament for the differential modulation of blood vessel endothelial
CC cell or lymphatic vessel endothelial cell growth or differentiation. The
CC lymphatic growth agent may also be used in manufacturing a medicament for
CC the treatment of hereditary lymphoedema resulting from a mutation in a
CC LEC gene or of other diseases involving the lymphatic vessels, such as
CC various inflammatory diseases and cancer metastasis via the lymphatic
CC system. The present sequence is that of a human LEC/BEC differentially
CC expressed protein which is related to the method of the invention. Note:
CC this sequence does not appear in the specification but was obtained by
CC the indexer using the source data given in table 14 of the specification.
XX
SQ Sequence 5737 AA;

Query Match 88.3%; Score 68; DB 7; Length 5737;
Best Local Similarity 91.7%; Pred. No. 6.1;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||
DB 3022 WSWSSCSRSCG 3033

RESULT 7
ABG21064
ID ABG21064 standard; protein; 9222 AA.
XX
AC ABG21064;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #21055.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS95251.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 51423; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 9222 AA;

Query Match 88.3%; Score 68; DB 4; Length 9222;
Best Local Similarity 91.7%; Pred. No. 9.2;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
|||
DB 2205 WSWSSCSRSCG 2216

RESULT 8

AAB72283
ID AAB72283 standard; protein; 997 AA.
XX
AC AAB72283;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human ADAMTS-7 amino acid sequence.
XX
KW ADAMTS-N; disintegrin; metalloprotease; thrombospondin type I motif;
tumour cachexia; inflammation; dermatosparaxis; EDS-VIIC; angiogenesis;
KW Ehlers-Danlos syndrome type VIIC; articular cartilage erosion; human;
metastasis; embryogenesis; egg implantation; chromosome 15; ADAMTS-7.
XX
OS Homo sapiens.
XX
PN WO200111074-A2.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-US021223.
XX
PR 06-AUG-1999; 99US-00369364.
XX
PA (CLEV-) CLEVELAND CLINIC FOUND.
PA (APTE/) APTE S S.
PA (HURS/) HURSKAINEN T L.
PA (HIRO/) HIROHATA S.
XX
PI Apte SS, Hurskainen TL, Hirohata S;
XX
DR WPI; 2001-159978/16.
DR N-PSDB; AAF63440.
XX
PT Murine and human 'A Disintegrin-like And Metalloprotease domain with
Thrombospondin type I motifs' proteins and the nucleic acids encoding
PT them, useful for treating e.g. tumors, inflammation and arthritis.
XX
PS Claim 15; Fig 4; 181pp; English.
XX
CC This invention relates to murine and human ADAMTS-N (A disintegrin-like
and metalloprotease domain with thrombospondin type I motifs) proteins,
CC designated ADAMTS-5, 6, 7, 8, 9, 10 and R1. Also included in the
CC invention are cDNA sequences encoding the proteins, and antibodies
CC specific for the proteins. The nucleic acid sequences and proteins may be
CC used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate ADAMTS-N expression. Disorders that may be treated
CC using the nucleic acids, proteins and antibodies include, for example
CC tumour cachexia, inflammation, dermatosparaxis in cattle or Ehlers-Danlos
CC syndrome type VIIC (EDS-VIIC) in humans, erosion of articular cartilage
CC in arthritic (both inflammatory and non-inflammatory) disease,
CC angiogenesis, tumour growth and metastases, and they may also be used for
CC controlling embryogenesis and implantation of fertilised eggs. The
CC present sequence represents human ADAMTS-7. The human ADAMTS-7 gene is
CC located on chromosome 15
XX
SQ Sequence 997 AA;

Query Match 84.4%; Score 65; DB 4; Length 997;
Best Local Similarity 83.3%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| |||||
Db 544 WSAWSICSRSCG 555

RESULT 9
ADJ69288
ID ADJ69288 standard; protein; 997 AA.
XX
AC ADJ69288;
XX

DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID1094.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 1094; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 997 AA;

Query Match 84.4%; Score 65; DB 7; Length 997;
Best Local Similarity 83.3%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| |||||
Db 544 WSAWSICSRSCG 555

RESULT 10
ABB60410
ID ABB60410 standard; protein; 1054 AA.
XX
AC ABB60410;
XX
DT 26-MAR-2002 (first entry)

Fri Apr 1 15:03:05 2005

XX Drosophila melanogaster polypeptide SEQ ID NO 8022.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
KW
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US009231.
PF
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR N-PSDB; ABL04513.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
PT
XX Disclosure; SEQ ID NO 8022; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1054 AA;
SQ
Query Match 84.4%; Score 65; DB 4; Length 1054;
Best Local Similarity 83.3%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WSGWSSCSRSCG 12
DB 629 WSEWSECSRSCG 640
RESULT 11
ADI28031
ID ADI28031 standard; protein; 1255 AA.
XX
AC ADI28031;
XX
DT 15-APR-2004 (first entry)
XX
DE ECMCAD protein 55022490CD1.
XX
KW nootropic; antisickling; antianemic; antitumor; anti-HIV; antiallergic;
KW antianemic; antiasthmatic; immunosuppressive; antiatherosclerotic;
KW dermatological; nephrotrophic; antigout; antithyroid; neuroprotective;
KW osteopathic; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW antiinflammatory; ophthalmological; anticonvulsant; antiparkinsonian;
KW antibacterial; virucide; tranquilizer; neuroleptic; antidiabetic;
KW cytostatic; hepatotropic; gene therapy;
KW human extracellular matrix and cell adhesion molecule; ECMCAD; diagnosis;
KW genetic disorder; adrenoleukodystrophy; Down's syndrome; cystic fibrosis;
KW Gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;
KW Wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;

KW AIDS; adult respiratory distress syndrome; allergy; anemia; asthma;
KW atherosclerosis; autoimmune hemolytic anemia; contact dermatitis;
KW Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;
KW osteoporosis; psoriasis; rheumatoid arthritis; scleroderma;
KW systemic lupus erythematosus; ulcerative colitis; uveitis;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; multiple sclerosis;
KW meningitis; periodic paralysis; mental disorder; mood; anxiety;
KW schizophrenia; amnesia; diabetic neuropathy; osteomyelitis;
KW osteoporosis; Paget's disease; osteonecrosis; osteoarthritis;
KW chondrosarcoma; giant cell tumor; psoriatic arthritis;
KW infectious arthritis; systemic sclerosis; cell proliferative disorder;
KW actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer;
KW adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.
XX
OS Homo sapiens.
XX WO200202634-A2.
PN
XX 10-JAN-2002.
PD
XX 29-JUN-2001; 2001WO-US021067.
PF
XX 30-JUN-2000; 2000US-0215454P.
PR 18-JUL-2000; 2000US-0219462P.
PR 12-OCT-2000; 2000US-0240106P.
PR 12-OCT-2000; 2000US-0240111P.
PR 27-OCT-2000; 2000US-0244021P.
PR 14-NOV-2000; 2000US-0248887P.
PR 16-NOV-2000; 2000US-0249570P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX Tang YT, Yue H, Azimzai Y, He A, Batra S, Lo TP, Nguyen DB;
XX Burrill JD, Marcus GA, Zingler KA, Gandhi AR, Lal P, Kearney L;
XX Burford N, Yao MG, Wallia NK, Elliot VS, Patterson C, Khan FA;
XX Baughn MR, Hafalia AJA, Policky JL, Au-Young J, Lu Y, Borowsky ML;
XX Lu DAM, Ramkumar J, Yang J, Gururajan R, Warren BA, Gietzen K;
XX Xu Y, Kallick DA, Lee EA, Thangavelu K, Delegeane AM, Lee S;
DR WPI; 2002-154732/20.
DR N-PSDB; ADI28067.
XX
XX Novel isolated human extracellular matrix and cell adhesion molecules
PT useful for treating, preventing connective tissue disorder e.g.
PT osteoporosis, Paget's disease, genetic disorder e.g. cystic fibrosis,
PT thalassemia.
XX
XX Claim 1; SEQ ID NO 23; 270pp; English.
PS
XX The invention relates to a novel isolated human extracellular matrix and
CC cell adhesion molecule (referred to as ECMCAD 1-36), its biologically
CC active or immunogenic fragment or a sequence comprising 90 % identity to
CC ECMCAD 1-36. The molecule is useful for screening a compound for
CC effectiveness as agonist or antagonist of itself. The protein and its
CC encoding nucleic acid are useful in the diagnosis, treatment and
CC prevention of genetic disorder such as adrenoleukodystrophy, Down's
CC syndrome, cystic fibrosis, Gaucher's disease, myotonic dystrophy, sickle
CC cell anemia, thalassemia, Wilms' tumor, etc, immunological disorders such
CC as acquired immunodeficiency syndrome (AIDS), adult respiratory distress
CC syndrome, allergies, anemia, asthma, atherosclerosis, autoimmune
CC hemolytic anemia, contact dermatitis, Goodpasture's syndrome, gout,
CC Grave's disease, multiple sclerosis, osteoporosis, psoriasis, rheumatoid
CC arthritis, scleroderma, systemic lupus erythematosus, ulcerative colitis,
CC uveitis, etc, a neurological disorder such as epilepsy, stroke,
CC Alzheimer's disease, Huntington's disease, Parkinson's disease, multiple
CC sclerosis, bacterial and viral meningitis, periodic paralysis, mental
CC disorders including mood, anxiety, and schizophrenic disorders, amnesia,
CC diabetic neuropathy, etc, connective tissue disorder such as
CC osteoporosis, Paget's disease, osteonecrosis, osteomyelitis,
CC chondrosarcoma, giant cell tumor, psoriatic arthritis, infectious
CC arthritis, systemic sclerosis, etc, and a cell proliferative disorder
CC such as actinic keratosis, atherosclerosis, hepatitis, psoriasis, cancers

CC including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, etc.
 CC This sequence represents one of the novel proteins.

XX
 SQ Sequence 1255 AA;

Query Match 84.4%; Score 65; DB 5; Length 1255;
 Best Local Similarity 83.3%; Pred. No. 3.9;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 |||||
 Db 113 WSAWSICSRSCG 124

RESULT 12

AAE00934
 ID AAE00934 standard; protein; 1686 AA.

XX AC AAE00934;

XX DT 04-JUL-2001 (first entry)

XX DE Human 27875 ADAM-TS (a disintegrin and metalloproteinase).

XX KW Human; ADAM-TS; A Disintegrin And Metalloproteinase; antiinflammatory;
 KW angiogenesis; bronchial asthma; Goodpasture's syndrome; metastasis;
 KW heart failure; cardiac hypertrophy; chronic ischaemic heart disease;
 KW sickle cell disease nephropathy; urinary tract obstruction; haemostatic;
 KW skeletal muscle disorder; myocardial infarction; blood vessel disorder;
 KW hypertension; atherosclerosis; syphilis; renal artery stenosis; mumps;
 KW gonorrhea; tuberculosis; vasculitis; spermatocytic seminoma; osteoporosis;
 KW rhabdomyosarcoma; glomerulonephritis; bone disorder; Paget's disease;
 KW rickets; osteomalacia; Hodgkin's disease; gene therapy; antibacterial;
 KW cardiant; tumour; thymoma; vasotropic; cytostatic; virucide.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..30
 FT /label= Signal_peptide
 FT Modified-site 6..8
 FT /note= "Protein kinase C phosphorylation site"
 FT Protein 31..1686
 FT /label= Human_mature_27875_ADAM-TS_protein
 FT Modified-site 55..60
 FT /note= "N-myristoylation site"
 FT Modified-site 73..75
 FT /note= "Protein kinase C phosphorylation site"
 FT Domain 78..93
 FT /note= "Crystallins beta and gamma Greek key motif"
 FT Modified-site 94..97
 FT /note= "N-glycosylation site"
 FT Modified-site 110..112
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 115..120
 FT /note= "N-myristoylation site"
 FT Modified-site 141..146
 FT /note= "N-myristoylation site"
 FT Modified-site 147..150
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 159..162
 FT /note= "Casein kinase II phosphorylation site"
 FT Binding-site 195..197
 FT /note= "Cell attachment sequence"
 FT Modified-site 214..217
 FT /note= "Casein kinase II phosphorylation site"
 FT Modified-site 214..216
 FT /note= "Protein kinase C phosphorylation site"
 FT Domain 244..259
 FT /label= Metalloproteinase_domain
 FT Modified-site 313..315
 FT /note= "Protein kinase C phosphorylation site"
 FT Modified-site 342..345

FT Modified-site
 FT /note= "Casein kinase II phosphorylation site"
 FT 342..344
 FT /note= "Protein kinase C phosphorylation site"
 FT 373..376
 FT /note= "Casein kinase II phosphorylation site"
 FT 379..384
 FT /note= "N-myristoylation site"
 FT 385..394
 FT /label= Zinc_binding_domain
 FT 401..404
 FT /note= "Casein kinase II phosphorylation site"
 FT 408..411
 FT /note= "Amidation site"
 FT 479..484
 FT /note= "N-myristoylation site"
 FT 488..567
 FT /label= Thrombospondin_domain
 FT 505..508
 FT /note= "Casein kinase II phosphorylation site"
 FT 513..518
 FT /note= "N-myristoylation site"
 FT 539..545
 FT /note= "Growth factor and cytokine metalloproteinase family signature 2 domain"
 FT 539..544
 FT /note= "N-myristoylation site"
 FT 541..592
 FT /label= Disintegrin_domain
 FT 542..592
 FT /label= Thrombospondin_domain
 FT 557..562
 FT /note= "N-myristoylation site"
 FT 569..571
 FT /note= "Protein kinase C phosphorylation site"
 FT 598..600
 FT /note= "Protein kinase C phosphorylation site"
 FT 605..608
 FT /note= "Casein kinase II phosphorylation site"
 FT 614..619
 FT /note= "N-myristoylation site"
 FT 667..672
 FT /note= "N-myristoylation site"
 FT 687..692
 FT /note= "Cytochrome C family heme-binding site"
 FT 688..693
 FT /note= "N-myristoylation site"
 FT 693..696
 FT /note= "N-glycosylation site"
 FT 703..706
 FT /note= "Casein kinase II phosphorylation site"
 FT 716..721
 FT /note= "N-myristoylation site"
 FT 740..747
 FT /note= "Tyrosine kinase phosphorylation site"
 FT 765..770
 FT /note= "N-myristoylation site"
 FT 774..779
 FT /note= "N-myristoylation site"
 FT 778..781
 FT /note= "N-glycosylation site"
 FT 825..868
 FT /label= Thrombospondin_domain
 FT 872..875
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT 901..903
 FT /note= "Protein kinase C phosphorylation site"
 FT 917..920
 FT /note= "Casein kinase II phosphorylation site"
 FT 949..994
 FT /label= Thrombospondin_domain
 FT 949..988
 FT /label= Thrombospondin_domain

FT	Modified-site	950. .953	/note= "N-glycosylation site"
FT	Modified-site	957. .960	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	962. .964	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	971. .974	/note= "N-glycosylation site"
FT	Modified-site	1005. .1010	/note= "N-myristoylation site"
FT	Binding-site	1006. .1009	/note= "Glycosaminoglycan attachment site"
FT	Modified-site	1011. .1014	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1035. .1037	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1039. .1044	/note= "N-myristoylation site"
FT	Modified-site	1192. .1195	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1263. .1268	/note= "N-myristoylation site"
FT	Modified-site	1263. .1252	/note= "N-myristoylation site"
FT	Modified-site	1308. .1311	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1358. .1363	/note= "N-myristoylation site"
FT	Modified-site	1370. .1372	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1385. .1387	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1397. .1400	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1412. .1415	/note= "N-glycosylation site"
FT	Domain	1415. .1463	/label= Thrombospondin_domain
FT	Modified-site	1419. .1422	/note= "N-glycosylation site"
FT	Modified-site	1440. .1443	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1440. .1442	/note= "Protein kinase C phosphorylation site"
FT	Domain	1466. .1521	/label= Thrombospondin_domain
FT	Modified-site	1470. .1473	/note= "N-glycosylation site"
FT	Modified-site	1483. .1486	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1483. .1485	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1517. .1522	/note= "N-myristoylation site"
FT	Modified-site	1528. .1531	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1528. .1530	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1546. .1549	/note= "Casein kinase II phosphorylation site"
FT	Modified-site	1592. .1597	/note= "N-myristoylation site"
FT	Modified-site	1599. .1601	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1606. .1609	/note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT	Modified-site	1620. .1622	/note= "Protein kinase C phosphorylation site"
FT	Modified-site	1625. .1630	

Query Match 84.4%; Score 65; DB 4; Length 1686;
Best Local Similarity 83.3%; Pred. No. 5;

	Matches	10;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	WSGWSSCSRSCG 12								
Db	544	WSAWSICSRSCG 555								
RESULT 13										
AAE00913										
ID	AAE00913	standard; protein; 1686 AA.								
XX	AC	AAE00913;								
XX	DT	04-JUL-2001 (first entry)								
XX	DE	Human 27875 ADAM-TS protein, alternative version.								
XX	KW	Human; ADAM-TS; A Disintegrin And Metalloproteinase; antiinflammatory; angiogenesis; bronchial asthma; Goodpasture's syndrome; metastasis; heart failure; cardiac hypertrophy; chronic ischaemic heart disease; sickle cell disease nephropathy; urinary tract obstruction; haemostatic; skeletal muscle disorder; myocardial infarction; blood vessel disorder; hypertension; atherosclerosis; vasculitis; renal artery stenosis; mumps; gonorrhea; tuberculosis; syphilis; spermatocytic seminoma; osteoporosis; rhabdomyosarcoma; glomerulonephritis; bone disorder; Paget's disease; rickets; osteomalacia; Hodgkin's disease; gene therapy; antibacterial; cardiant; tumour; thymoma; vasotropic; cytostatic; virucide.								
XX	OS	Homo sapiens.								
XX	Key	Location/Qualifiers								
FT	Peptide	1. .30								
FT	Modified-site	/label= Signal_peptide								
FT	Protein	6. .8								
FT	Modified-site	/note= "Protein kinase C phosphorylation site"								
FT	Modified-site	31. .1686								
FT	Modified-site	/label= Human_mature_27875_ADAM-TS_protein								
FT	Modified-site	55. .60								
FT	Modified-site	/note= "N-myristoylation site"								
FT	Domain	73. .75								
FT	Modified-site	/note= "protein kinase C phosphorylation site"								
FT	Modified-site	78. .93								
FT	Modified-site	/note= "Crystallins beta and gamma Greek key motif"								
FT	Modified-site	94. .97								
FT	Modified-site	/note= "N-glycosylation site"								
FT	Modified-site	110. .112								
FT	Modified-site	/note= "Protein kinase C phosphorylation site"								
FT	Modified-site	115. .120								
FT	Modified-site	/note= "N-myristoylation site"								
FT	Modified-site	141. .146								
FT	Modified-site	/note= "N-myristoylation site"								
FT	Modified-site	147. .150								
FT	Modified-site	/note= "Casein kinase II phosphorylation site"								
FT	Modified-site	159. .162								
FT	Modified-site	/note= "Casein kinase II phosphorylation site"								
FT	Binding-site	195. .197								
FT	Modified-site	/note= "Cell attachment sequence"								
FT	Modified-site	214. .217								
FT	Modified-site	/note= "Casein kinase II phosphorylation site"								
FT	Modified-site	214. .216								
FT	Modified-site	/note= "Protein kinase C phosphorylation site"								
FT	Domain	244. .259								
FT	Modified-site	/label= Metalloproteinase_domain								
FT	Modified-site	313. .315								
FT	Modified-site	/note= "Protein kinase C phosphorylation site"								
FT	Modified-site	342. .345								
FT	Modified-site	/note= "Casein kinase II phosphorylation site"								
FT	Modified-site	342. .344								
FT	Modified-site	/note= "Protein kinase C phosphorylation site"								
FT	Modified-site	373. .376								
FT	Modified-site	/note= "Casein kinase II phosphorylation site"								
FT	Modified-site	379. .384								
FT	Modified-site	/note= "N-myristoylation site"								

FT Domain 385. .394 /label= Zinc_binding_domain
 FT Modified-site 401. .404 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 408. .411 /note= "Amidation site"
 FT Modified-site 479. .484 /note= "N-myristoylation site"
 FT Domain 488. .567 /label= Thrombospondin_domain
 FT Modified-site 505. .508 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 513. .518 /note= "N-myristoylation site"
 FT Domain 539. .545 /note= "Growth factor and cytokine metalloproteinase family signature 2 domain"
 FT Modified-site 539. .544 /note= "N-myristoylation site"
 FT Domain 541. .592 /label= Disintegrin_domain
 FT Domain 542. .592 /label= Thrombospondin_domain
 FT Modified-site 557. .562 /note= "N-myristoylation site"
 FT Modified-site 569. .571 /note= "Protein kinase C phosphorylation site"
 FT Misc-difference 596 /label= Unknown
 FT Modified-site 598. .600 /note= "Encoded by CRC"
 FT Modified-site 605. .608 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 614. .619 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 667. .672 /note= "N-myristoylation site"
 FT Binding-site 687. .692 /note= "N-myristoylation site"
 FT Modified-site 688. .693 /note= "Cytochrome C family heme-binding site"
 FT Modified-site 693. .696 /note= "N-myristoylation site"
 FT Modified-site 703. .706 /note= "N-glycosylation site"
 FT Modified-site 716. .721 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 740. .747 /note= "N-myristoylation site"
 FT Modified-site 765. .770 /note= "Tyrosine kinase phosphorylation site"
 FT Modified-site 774. .779 /note= "N-myristoylation site"
 FT Modified-site 778. .781 /note= "N-myristoylation site"
 FT Domain 825. .868 /label= Thrombospondin_domain
 FT Modified-site 872. .875 /note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 901. .903 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 917. .920 /note= "Casein kinase II phosphorylation site"
 FT Domain 949. .994 /label= Thrombospondin_domain
 FT Domain 949. .988 /label= Thrombospondin_domain
 FT Modified-site 950. .953 /note= "N-glycosylation site"
 FT Modified-site 957. .960 /note= "Casein kinase II phosphorylation site"

FT Modified-site 962. .964 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 971. .974 /note= "N-glycosylation site"
 FT Modified-site 1005. .1010 /note= "N-myristoylation site"
 FT Binding-site 1006. .1009 /note= "Glycosaminoglycan attachment site"
 FT Modified-site 1011. .1014 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 1035. .1037 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 1039. .1044 /note= "N-myristoylation site"
 FT Modified-site 1192. .1195 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 1263. .1268 /note= "N-myristoylation site"
 FT Modified-site 1263. .1252 /note= "N-myristoylation site"
 FT Modified-site 1308. .1311 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 1358. .1363 /note= "N-myristoylation site"
 FT Modified-site 1370. .1372 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 1385. .1387 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 1397. .1400 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 1412. .1415 /note= "N-glycosylation site"
 FT Domain 1415. .1463 /label= Thrombospondin_domain
 FT Modified-site 1419. .1422 /note= "N-glycosylation site"
 FT Modified-site 1440. .1443 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 1440. .1442 /note= "Protein kinase C phosphorylation site"
 FT Domain 1466. .1521 /label= Thrombospondin_domain
 FT Modified-site 1470. .1473 /note= "N-glycosylation site"
 FT Modified-site 1483. .1486 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 1483. .1485 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 1517. .1522 /note= "N-myristoylation site"
 FT Modified-site 1528. .1531 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 1528. .1530 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 1546. .1549 /note= "Casein kinase II phosphorylation site"
 FT Modified-site 1592. .1597 /note= "N-myristoylation site"
 FT Modified-site 1599. .1601 /note= "Protein kinase C phosphorylation site"
 FT Modified-site 1606. .1609 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

Query Match 84.4%; Score 65; DB 4; Length 1686;
 Best Local Similarity 83.3%; Pred. No. 5;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
 Db 544 WSAWSICSRSCG 555

Fri Apr 1 15:03:05 2005

RESULT 14
AAB74944
ID AAB74944 standard; protein; 1686 AA.
XX
XX AC AAB74944;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human ADAM type metal protease MDTs1 protein SEQ ID NO:1.
XX
KW Human; a disintegrin and metalloprotease type metal protease; MDTs1;
KW MDTs2; MDTs3; ADAM type metal protease; cytosolic; antiarthritic;
KW cancer; arthritis; arthrosis deformans.
XX
OS Homo sapiens.
XX
PN JP2001008687-A.
XX
PD 16-JAN-2001.
XX
PF 25-JUN-1999; 99JP-00180973.
XX
PR 25-JUN-1999; 99JP-00180973.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
XX WPI; 2001-285362/30.
DR N-PSDB; AAF82149.
XX
XX New metal protease and metal protease gene, for use as a drug for
PT cancers, arthritis and arthrosis deformans.
XX
PS Claim 1; Page 12-17; 31pp; Japanese.
XX
CC The present sequence represents a disintegrin and metalloprotease (ADAM)
CC type metal protease designated MDTs1, isolated from human. MDTs proteins
CC have cytosolic and antiarthritic activities. They can be used as a drug
CC for cancers, arthritis and arthrosis deformans
XX
SQ Sequence 1686 AA;

Query Match 84.4%; Score 65; DB 4; Length 1686;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12
||| ||| ||| ||| |||
Db 544 WSAWSICSRSCG 555

RESULT 15
ADJ58902
ID ADJ58902 standard; protein; 1686 AA.

XX
AC ADJ58902;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human ADAM-TS protein, 27875.
XX
KW 27875; 22025; 27420; 17906; 16319; 55092; 10218; cancer;
KW cellular proliferation; cellular differentiation; immune disorder;
KW cardiovascular disorder; endothelial cell disorder;
KW haematopoietic disorder; blood vessel disorder; brain disorder; pain;
KW metabolic disorder; liver disorder; platelet disorder; gene therapy;
KW human; ADAM-TS; enzyme.

XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= Signal_peptide 31..1686

FT Domain /note= "Human mature ADAM-TS protein"
FT 244..259
FT /note = Metalloprotease domain
FT 385..394
FT /note = Zinc-binding domain
FT 541..592
FT /note = Disintegrin domain
FT 542..592
FT /note = S thrombospondin domain
FT Misc-difference 596
FT /note= "Encoded by CRC"
FT 825..868
FT /note = S thrombospondin domain
FT 949..988
FT /note = S thrombospondin domain
FT 1415..1463
FT /note = S thrombospondin domain
FT 1466..1521
FT /note = S thrombospondin domain
FT Misc-difference 1479
FT /note= "Encoded by GAC"
FT 1511
FT Misc-difference 1511
FT /note= "Encoded by CAT"
XX
PN US2004006016-A1.
XX
PD 08-JAN-2004.
XX
PF 11-MAR-2003; 2003US-00386414.
XX
PR 11-JUN-1999; 99US-00330970.
PR 25-OCT-1999; 99US-00426282.
PR 16-MAY-2000; 2000US-00571689.
PR 22-SEP-2000; 2000US-00668266.
PR 28-NOV-2000; 2000US-00724599.
PR 07-DEC-2000; 2000US-0254037P.
PR 10-APR-2001; 2001US-00833082.
PR 16-MAY-2001; 2001US-00860193.
PR 31-OCT-2001; 2001US-0335044P.
PR 06-DEC-2001; 2001US-00010943.
PR 29-OCT-2002; 2002US-00283023.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kapeller-Libermann R, White D, Robison KE, Macbeth KJ, Carroll JM;
PI Cook WJ, Meyers RE, Chun M, Williamson MJ;
PI
XX WPI; 2004-081738/08.
DR N-PSDB; ADJ58901.
XX
XX New isolated 27875, 22025, 27420, 17906, 16319, 55092, or 10218 nucleic
PT acid molecules, useful for diagnosing or treating cancer, pain, or
PT immune, endothelial cell, hematopoietic, blood vessel, brain, metabolic
PT and liver disorders.
XX
PS Claim 4; SEQ ID NO 2; 245pp; English.
XX
XX The present invention relates to an isolated 27875, 22025, 27420, 17906,
CC 16319, 55092, or 10218 nucleic acid molecule. The invention is useful for
CC diagnosing or treating cancer or aberrant cellular proliferation and/or
CC differentiation, immune disorders, heart disorders, cardiovascular
CC disorders including endothelial cell disorders, haematopoietic disorders,
CC blood vessel disorders, brain disorders, pain and metabolic disorders,
CC liver disorders and platelet disorders. The invention is also useful in
CC gene therapy. The present sequence is human ADAM-TS protein.
XX
SQ Sequence 1686 AA;

Query Match 84.4%; Score 65; DB 8; Length 1686;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WSGWSSCSRSCG 12

Db 544 WSAWSICSRSCG 555

Search completed: April 1, 2005, 13:54:26
Job time : 85.7391 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:24:31 ; Search time 75.6522 Seconds
(without alignments)
81.226 Million cell updates/sec

Title: US-09-462-909D-7
Perfect score: 62
Sequence: 1 WSXWSXCSXXCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:
1: uniprot_prot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	93.5	504	Q69HL7	Q69hl7 ciona intes
2	58	93.5	3869	Q86PQ3	Q86pq3 cryptospori
3	57	91.9	238	Q76510	Q76510 cryptospori
4	57	91.9	257	Q966K7	Q966k7 caenorhabdi
5	57	91.9	872	Q22580	Q22580 caenorhabdi
6	57	91.9	1077	1 SM5A_MOUSE	Q62217 mus musculu
7	57	91.9	1093	Q7QC32	Q7qc32 anopheles g
8	57	91.9	4998	Q8CG65	Q8cg65 mus musculu
9	57	91.9	5141	Q700K0	Q700k0 ratu
10	56	90.3	106	Q43982	Q43982 cryptospori
11	56	90.3	156	Q8MXY6	Q8mxy6 cryptospori
12	56	90.3	168	Q9GZ21	Q9gz21 cryptospori
13	56	90.3	168	Q9GZ22	Q9gz22 cryptospori
14	56	90.3	168	Q9GZ23	Q9gz23 cryptospori
15	56	90.3	192	Q7JN23	Q7jn23 cryptospori
16	56	90.3	449	Q8QFV1	Q8qfv1 xenopus lae
17	56	90.3	461	Q95S22	Q95s22 drosophila
18	56	90.3	549	Q8T988	Q8t988 drosophila
19	56	90.3	612	Q6ZQ96	Q6zq96 mus musculu
20	56	90.3	628	Q7KRF4	Q7krf4 drosophila
21	56	90.3	654	Q19284	Q19284 caenorhabdi
22	56	90.3	656	Q86PQ8	Q86pq8 cryptospori
23	56	90.3	660	Q23832	Q23832 cryptospori
24	56	90.3	687	Q23729	Q23729 cryptospori
25	56	90.3	724	Q04588	Q04588 elmeria max
26	56	90.3	763	Q9XZD0	Q9xzd0 drosophila
27	56	90.3	839	Q8ML26	Q8ml26 drosophila
28	56	90.3	867	1 SSPO_BOVIN	P98167 bos taurus
29	56	90.3	880	Q8MSF8	Q8msf8 drosophila
30	56	90.3	880	Q9VKV3	Q9vkv3 drosophila
31	56	90.3	997	1 ATS7_HUMAN	Q9ukp4 homo sapien

32	56	90.3	1081	2 Q9U631	Q9u631 drosophila
33	56	90.3	1089	2 Q8T3A0	Q8t3a0 ciona intes
34	56	90.3	1091	2 Q7YU67	Q7yu67 drosophila
35	56	90.3	1093	2 Q9VTT0	Q9vtt0 drosophila
36	56	90.3	1282	2 Q68FL1	Q68fl1 mus musculu
37	56	90.3	1361	2 Q6PD18	Q6pd18 mus musculu
38	56	90.3	1461	2 Q8MYA8	Q8mya8 caenorhabdi
39	56	90.3	1522	1 BAI3_HUMAN	Q60242 homo sapien
40	56	90.3	1522	1 BAI3_MOUSE	Q80zf8 mus musculu
41	56	90.3	1641	2 Q68SA9	Q68sa9 mus musculu
42	56	90.3	1668	2 Q69ZU6	Q69zu6 mus musculu
43	56	90.3	1686	2 Q6P7J9	Q6p7j9 homo sapien
44	56	90.3	1905	2 Q9XTP6	Q9xtp6 plasmodium
45	56	90.3	2098	2 Q25757	Q25757 plasmodium

ALIGNMENTS

RESULT 1
Q69HL7
ID Q69HL7 PRELIMINARY; PRT; 504 AA.
AC Q69HL7;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE HrtT-1-like (Fragment).
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23047825; PubMed=14686582;
RA Terajima D., Yamada S., Uchino R., Ikawa S., Ikeda M., Shida K.,
RA Arai Y., Wang H.G., Satoh N., Satake M.;
RT "Identification and sequence of seventy-nine new transcripts expressed
in hemocytes of Ciona intestinalis, three of which may be involved in
characteristic cell-cell communication.";
RL DNA Res. 10:203-212(2003).
DR EMBL; AY261898; AAP91764.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002413; V5_allergen.
DR Pfam; PF00188; SCP; 1.
DR Pfam; PF00090; TSP 1; 4.
DR PRINTS; PR00838; V5ALLERGEN.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS01009; CRISP_1; 1.
DR PROSITE; PS01010; CRISP_2; UNKNOWN 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00092; TSP1; 5.
FT NON_TER 1
FT NON_TER 504
SQ SEQUENCE 504 AA; 55337 MW; 305F43A92B850F29 CRC64;
Query Match 93.5%; Score 58; DB 2; Length 504;
Best Local Similarity 66.7%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
|||
Db 477 WSAWSACSTSCG 488
|||

RESULT 2
Q86PQ3
ID Q86PQ3 PRELIMINARY; PRT; 3869 AA.

AC Q86PQ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE TSPI domain-containing protein TSP2 precursor.
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22326344; PubMed=12438378;
RX DOI=10.1128/IAI.70.12.6987-6995.2002;
RA Deng M., Templeton T.J., London N.R., Bauer C., Schroeder A.A.,
RA Abrahamson M.S.;
RT "Cryptosporidium parvum genes containing thrombospondin type 1
RT domains";
RL Infect. Immun. 70:6987-6995(2002).
RL EMBL; AY190984; AAO39046.1; -.
DR HSSP; P07996; 1LSL.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR000800; Notch_region.
DR InterPro; IPR003582; ShKT.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00066; Notch; 2.
DR Pfam; PF01549; ShTK; 5.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00090; TSP_1; 10.
DR Pfam; SM00032; CCP; 2.
DR SMART; SM00004; NL; 6.
DR SMART; SM00254; ShKT; 5.
DR SMART; SM00209; TSPI; 11.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN 3.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS50092; TSPI; 10.
KW Signal.
FT SIGNAL
SQ SEQUENCE 3869 AA; 429514 MW; 1F4851B7B0787B87 CRC64;

Query Match 93.5%; Score 58; DB 2; Length 3869;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 386 WSSWSCSTSCG 397

RESULT 3
O76510 PRELIMINARY; PRT; 238 AA.
AC O76510;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C3;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Moredu;
RA Spano F., Putignani L., Crisanti A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF073838; AAC26812.1; -.
DR HSSP; P07996; 1LSL.
DR InterPro; IPR002086; Aldehyd dehydrog.

DR InterPro; IPR000884; TSPI.
DR Pfam; PF00090; TSP_1; 3.
DR SMART; SM00209; TSPI; 3.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS50092; TSPI; 3.
FT NON_TER 1
FT NON_TER 238
SQ SEQUENCE 238 AA; 26307 MW; 28242DE88F62C5A2 CRC64;

Query Match 91.9%; Score 57; DB 2; Length 238;
Best Local Similarity 66.7%; Pred. No. 0.35;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 47 WSSWSACSXSCG 58

RESULT 4
Q966K7 PRELIMINARY; PRT; 257 AA.
AC Q966K7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein F14H12.3.
GN Name=F14H12.3; ORFNames=F14H12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Gattung S., R Wilson.;
RT "The sequence of C. elegans cosmid F14H12.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006630; AAK68325.1; -.
DR HSSP; P07996; 1LSL.
DR WormBase; WBGene00017471; F14H12.3.

```
DR WormPep; F14H12.3; CE07063.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000885; TSP1.
DR Pfam; PF00090; TSP1; 3.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS00092; TSP1; 3.
KW Hypothetical protein.
SQ SEQUENCE 257 AA; 26512 MW; 9B052A0D07F2BEFF CRC64;

Query Match          91.9%; Score 57; DB 2; Length 257;
Best Local Similarity 66.7%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 145 WSSWSACSXVTCG 156

RESULT 5
Q22580 PRELIMINARY; PRT; 872 AA.
AC Q22580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T19D2.1.
GN Name=T19D2.1; ORFNames=T19D2.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid T19D2."
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U42846; AAA83600.2; -.
DR PIR; T16892; T16892.
DR HSSP; P07996; ILSL.
DR WormBase; WBGene00020567; T19D2.1.
DR WormPep; T19D2.1; CE30185.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP1; 4.
DR SMART; SM00209; TSP1; 4.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50092; TSP1; 4.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.

SQ SEQUENCE 872 AA; 98040 MW; 1BA1D480AEF0ED15 CRC64;

Query Match          91.9%; Score 57; DB 2; Length 872;
Best Local Similarity 66.7%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 831 WSSWSSCSTKCG 842

RESULT 6
SM5A_MOUSE
ID SM5A_MOUSE STANDARD; PRT; 1077 AA.
AC Q62217;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 5A precursor (Semaphorin F) (Sema F).
GN Name=Sema5a; Synonyms=Semaf, SemF;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI;
RX MEDLINE=96414430; PubMed=8817451; DOI=10.1016/0925-4773(96)00525-4;
RA Adams R.H.; Betz H.; Pueschel A.W.;
RT "A novel class of murine semaphorins with homology to thrombospondin
is differentially expressed during early embryogenesis."
RL Mech. Dev. 57:33-45(1996).
CC -1- FUNCTION: May act as positive axonal guidance cues.
CC -1- SUBUNIT: Binds PLXNB3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: In adult, detected in liver, brain, kidney,
heart, lung and spleen.
CC -1- DEVELOPMENTAL STAGE: Differentially expressed in embryonic and
adult tissues. Its abundance decreases from E10 to birth.
CC -1- SIMILARITY: Belongs to the semaphorin family.
CC -1- SIMILARITY: Contains 1 Sema domain.
CC -1- SIMILARITY: Contains 7 TSP type-1 domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X97817; CAA66397.1; -.
DR HSSP; P07996; ILSL.
DR MGD; MGI:107556; Sema5a.
DR GO; GO:0016021; C:integral to membrane; IDA.
DR GO; GO:0008046; F:axon guidance receptor activity; IDA.
DR GO; GO:0007411; P:axon guidance; IMP.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP_1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR SMART; SM00209; TSP1; 6.
DR PROSITE; PS51004; SEMA; 1.
DR PROSITE; PS50092; TSP1; 6.
KW Developmental protein; Glycoprotein; Multigene family; Neurogenesis;
Repeat; Signal; Transmembrane.
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FT SIGNAL 1 21 Potential.
FT CHAIN 22 1077 Semaphorin 5A.
FT DOMAIN 22 971 Extracellular (Potential).
FT TRANSMEM 972 992 Potential.
FT DOMAIN 993 1077 Cytoplasmic (Potential).
FT DOMAIN 35 484 Sema.
FT DOMAIN 540 593 TSP type-1 1.
FT DOMAIN 595 651 TSP type-1 2.
FT DOMAIN 653 702 TSP type-1 3.
FT DOMAIN 707 765 TSP type-1 4.
FT DOMAIN 784 839 TSP type-1 5.
FT DOMAIN 841 896 TSP type-1 6.
FT DOMAIN 897 944 TSP type-1 7.
FT DISULFID 104 114 By similarity.
FT DISULFID 131 140 By similarity.
FT DISULFID 278 320 By similarity.
FT DISULFID 487 504 By similarity.
FT DISULFID 496 513 By similarity.
FT CARBOHYD 147 168 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 168 177 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 227 277 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 277 277 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 323 323 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 367 367 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 717 717 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 933 933 N-linked (GlcNAc. .) (Potential).
FT SEQUENCE 1077 AA; 120826 MW; EDABODDDA42789FF CRC64;

Query Match 91.9%; Score 57; DB 1; Length 1077;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
   |||||
Db 847 WSSWSKCSATCG 858

RESULT 7
Q7QC32 PRELIMINARY; PRT; 1093 AA.
ID Q7QC32
AC Q7QC32;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EbiP1179 (Fragment).
GN Name=ebiG1179; ORFNames=ENSANGG0000001015;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OC NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB01008859; EAA07529.1; -.
DR HSSP; Q92854; IOLZ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002165; F:plexin_repeat.
DR InterPro; IPR001627; Sema.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR Pfam; PF00090; TSP 1; 5.
DR PRINTS; PR01705; TSP1REPEAT.
DR PROSITE; PS50092; TSP1; 5.

QY 1 WSXWSXCSXXCG 12
   |||||
Db 847 WSSWSKCSATCG 858

RESULT 8
Q8CG65 PRELIMINARY; PRT; 4998 AA.
ID Q8CG65
AC Q8CG65;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SCO-spondin.
GN Name=Scospondin; Synonyms=sco-spondin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Goncalves N., Simon-Chazottes D., Creveaux I., Meinzel A.,
RA Guenet J-L., Meinzel R.;
RA "Mouse SCO-spondin, a gene of the thrombospondin type 1 repeat (TSR)
RT superfamily expressed in the brain.";
RL Gene 312:263-270(2003).
CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ491857; CAD42654.1; -.
DR HSSP; P01130; IAJJ.
DR MGD; MGI:2674311; Scospondin.
DR GO; GO:0005737; C:cytoplasm; IC.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys knot C.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FA58 C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR008037; Prot_inh_PMP.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5 F8 type C; 1.
DR Pfam; PF00057; Ldl_recept_a; 10.
DR Pfam; PF05375; Pacifastin_I; 1.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP 1; 25.
DR Pfam; PF00093; VWC; 1.
DR Pfam; PF00094; VWD; 2.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00068; GHB; 1.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSP1; 25.
DR SMART; SM00214; VWC; 4.
DR SMART; SM00216; VWD; 2.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS01225; CTCK 2; 1.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS50022; FA58C 3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.
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FT NON_TER 1 1
FT NON_TER 1093 1093
SQ SEQUENCE 1093 AA; 118842 MW; 2DB86BEC7CB42230 CRC64;

Query Match 91.9%; Score 57; DB 2; Length 1093;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
   |||||
Db 586 WSAWSACSQTG 597

RESULT 8
Q8CG65 PRELIMINARY; PRT; 4998 AA.
ID Q8CG65
AC Q8CG65;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SCO-spondin.
GN Name=Scospondin; Synonyms=sco-spondin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Goncalves N., Simon-Chazottes D., Creveaux I., Meinzel A.,
RA Guenet J-L., Meinzel R.;
RA "Mouse SCO-spondin, a gene of the thrombospondin type 1 repeat (TSR)
RT superfamily expressed in the brain.";
RL Gene 312:263-270(2003).
CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ491857; CAD42654.1; -.
DR HSSP; P01130; IAJJ.
DR MGD; MGI:2674311; Scospondin.
DR GO; GO:0005737; C:cytoplasm; IC.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys knot C.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FA58 C.
DR InterPro; IPR001545; Gly_hormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR008037; Prot_inh_PMP.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5 F8 type C; 1.
DR Pfam; PF00057; Ldl_recept_a; 10.
DR Pfam; PF05375; Pacifastin_I; 1.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP 1; 25.
DR Pfam; PF00093; VWC; 1.
DR Pfam; PF00094; VWD; 2.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00068; GHB; 1.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSP1; 25.
DR SMART; SM00214; VWC; 4.
DR SMART; SM00216; VWD; 2.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS01225; CTCK 2; 1.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS50022; FA58C 3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.
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DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 10.
DR PROSITE; PS50092; TSP1; 25.
DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
DR PROSITE; PS50184; VWFC_2; 2.
SQ SEQUENCE 4998 AA; 535028 MW; DA2ABA8DA47DF225 CRC64;

Query Match          91.9%; Score 57; DB 2; Length 4998;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Qy 1 WSXWSXCSCXXCG 12
Db 4012 WSAWSCSHSCG 4023

RESULT 9
Q700K0
ID Q700K0 PRELIMINARY; PRT; 5141 AA.
AC Q700K0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE SCO-spondin.
GN Name=sco-spondin; Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Meinzel O.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
DR EMBL; AJ629845; CAP33425.1; -.
DR HSSP; P01130; 1AJJ.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011489; EMI.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR01545; Gly_HormoneB.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR006552; VWC_out.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF07546; EMI; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00057; LdI_recept_a; 8.
DR Pfam; PF01826; TIL; 10.
DR Pfam; PF00090; TSP_1; 25.
DR Pfam; PF00093; VWC; 1.
DR Pfam; PF00094; VWD; 3.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00192; LDLa; 10.
DR SMART; SM00209; TSP1; 25.
DR SMART; SM00214; VWC; 5.
DR SMART; SM00215; VWC_out; 9.
DR SMART; SM00216; VWD; 3.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_2.
DR PROSITE; PS50022; FA58C_3; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_2.
DR PROSITE; PS01209; LDLRA_1; 8.
DR PROSITE; PS50068; LDLRA_2; 10.
DR PROSITE; PS50092; TSP1; 24.
DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
DR PROSITE; PS50184; VWFC_2; 2.
SQ SEQUENCE 5141 AA; 550644 MW; 1772AE67F02CA5E3 CRC64;

Query Match          91.9%; Score 57; DB 2; Length 5141;
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Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Qy 1 WSXWSXCSCXXCG 12
Db 4161 WSAWSCSHSCG 4172

RESULT 10
O43982
ID O43982 PRELIMINARY; PRT; 106 AA.
AC O43982;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE TRAP-C1 (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P12;
RX MEDLINE=98443215; PubMed=9769250; DOI=10.1006/expr.1998.4324;
RA Spano F., Putignani L., Guida S., Crisanti A.;
RT "Cryptosporidium parvum: PCR-RFLP analysis of the TRAP-C1
RT (Thrombospondin-related adhesive protein of Cryptosporidium-1) gene
RT discriminates between two alleles differentially associated with
RT parasite isolates of animal and human origin.";
RL Exp. Parasitol. 90:195-198(1998).
DR EMBL; AF033828; AAB92609.1; -.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 1.
DR SMART; SM00209; TSP1; 2.
DR PROSITE; PS50092; TSP1; 2.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11771 MW; 34D970D252058136 CRC64;

Query Match          90.3%; Score 56; DB 2; Length 106;
Best Local Similarity 66.7%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

Qy 1 WSXWSXCSCXXCG 12
Db 72 WSEWSDCSTSCG 83

RESULT 11
Q8MXY6
ID Q8MXY6 PRELIMINARY; PRT; 156 AA.
AC Q8MXY6;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Thrombospondin related adhesive protein (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HNJ-1;
RA Satoh M., Kimata I., Iseki M., Nakai Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB089293; BAC07243.1; -.
DR HSSP; P07996; 1LSL.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 1.
DR SMART; SM00209; TSP1; 2.
DR PROSITE; PS50092; TSP1; 2.
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DR HSP; P07996; 1LSL.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 2.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 18698 MW; 2D02BC437C2AA44D CRC64;

Query Match 90.3%; Score 56; DB 2; Length 168;
Best Local Similarity 66.7%; Pred.No. 0.37;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
   ||| ||| |||
Db 85 WSEWSDCSTSCG 96

RESULT 14
Q9GZ23 PRELIMINARY; PRT; 168 AA.
ID Q9GZ23
AC Q9GZ23;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thrombospondin-related adhesive protein (Fragment).
GN Name=TRAP-C1;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20389602; PubMed=10930736;
RA Pedraza-Diaz S.; Amar C.; McLauchlin J.;
RT "The identification and characterisation of an unusual genotype of
RT Cryptosporidium from human faeces as Cryptosporidium meleagridis.";
RL FEMS Microbiol. Lett. 189:189-194(2000).
DR EMBL; AF248744; AAGO1093.1; -.
DR HSP; P07996; 1LSL.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 2.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 18614 MW; F2AD32849A8B5E9C CRC64;

Query Match 90.3%; Score 56; DB 2; Length 168;
Best Local Similarity 66.7%; Pred.No. 0.37;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
   ||| ||| |||
Db 85 WSEWSDCSTSCG 96

RESULT 15
Q7JN23 PRELIMINARY; PRT; 192 AA.
ID Q7JN23
AC Q7JN23;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TRAP-C1 (Thrombospondin related adhesive protein) (Fragment).
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP SEQUENCE FROM N.A.
RA Spano F.S.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.

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DR EMBL; X77587; CAA54690.1; -.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP 1; 2.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS50092; TSP1; 3.
FT NON_TER 1
FT NON_TER 192 192
SQ SEQUENCE 192 AA; 21229 MW; B90CF7BDA2579612 CRC64;

Query Match 90.3%; Score 56; DB 2; Length 192;
Best Local Similarity 66.7%; Pred. No. 0.42;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WSXWSXCSCXXCG 12
|||
Db 80 WSEWSDCSTSCG 91

Search completed: April 1, 2005, 13:59:21
Job time : 78.6522 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:43:07 ; Search time 16.6957 Seconds
(without alignments)
69.156 Million cell updates/sec

Title: US-09-462-909D-7
Perfect score: 62
Sequence: 1 WSXWSXCSXXCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	91.9	860	2 T16892	hypothetical prote
2	56	90.3	654	2 T29247	hypothetical prote
3	56	90.3	724	2 A48569	antigen Em100 - Ei
4	56	90.3	984	2 T00326	hypothetical prote
5	56	90.3	1444	2 T18856	angiogenesis inhib
6	56	90.3	1522	2 T00028	brain-specific ang
7	56	90.3	2098	2 T18397	protein CTRP - mal
8	55	88.7	788	2 T25061	hypothetical prote
9	55	88.7	803	2 A47723	F-spondin precursor
10	55	88.7	807	2 A38152	F-spondin - rat
11	55	88.7	957	2 T15976	hypothetical prote
12	55	88.7	1170	1 TSHUP1	thrombospondin 1 p
13	55	88.7	1170	2 A40558	thrombospondin 1 p
14	55	88.7	1172	1 TSHUP2	thrombospondin 2 p
15	55	88.7	1172	2 A42587	thrombospondin 2 p
16	55	88.7	1178	1 A39804	thrombospondin pre
17	55	88.7	1184	2 T09484	cartilage intermed
18	55	88.7	1584	2 T00026	brain-specific ang
19	54	87.1	805	2 T34212	hypothetical prote
20	54	87.1	1572	2 T00027	brain-specific ang
21	53	85.5	206	2 A45517	coccidioides-relate
22	53	85.5	610	2 T16761	hypothetical prote
23	53	85.5	712	2 A45638	immunodominant mic
24	53	85.5	1074	2 JC5928	semaphorin F prece
25	52	83.9	1059	2 T22545	hypothetical prote
26	51	82.3	123	2 S49108	TRAP-C2 protein -
27	51	82.3	551	2 T16557	hypothetical prote
28	51	82.3	651	2 T19477	hypothetical prote
29	51	82.3	919	2 T32541	unc-5 protein - Ca

30	51	82.3	947	1 B44294	unc-5 protein, lon
31	51	82.3	1360	2 T33922	hypothetical prote
32	50	80.6	559	2 S04531	thrombospondin-rel
33	50	80.6	574	2 A46283	sporozoite surface
34	50	80.6	736	2 T19366	hypothetical prote
35	49	79.0	2761	2 T21064	hypothetical prote
36	47	75.8	324	2 T32570	hypothetical prote
37	47	75.8	2165	2 T21371	hypothetical prote
38	46	74.2	469	1 S29126	properdin precursor
39	46	74.2	550	2 T47158	hypothetical prote
40	46	74.2	826	2 A45559	sporozoite surface
41	46	74.2	837	2 T00355	hypothetical prote
42	46	74.2	951	2 T00017	gene ADAMTS-1 prot
43	45	72.6	951	2 T00260	hypothetical prote
44	44	71.0	152	2 D89753	protein F11C7.2 [i
45	44	71.0	437	2 S05478	properdin - mouse

ALIGNMENTS

RESULT 1

T16892
hypothetical protein T19D2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16892
R;Bentley, D.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19D2.
A;Reference number: Z18599
A;Accession: T16892
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-860 <BEN>
A;Cross-references: UNIPROT:Q22580; EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA8360
C;Genetics:
A;Gene: CESP:T19D2.1
A;Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 582/3

Query Match 91.9%; Score 57; DB 2; Length 860;
Best Local Similarity 66.7%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	WSXWSXCSXXCG 12
DB	831	WSSWSSCSTKCG 842

RESULT 2

T29247
hypothetical protein F09F9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29247
R;Minx, P.; Hawkins, J.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F09F9.
A;Reference number: Z20594
A;Accession: T29247
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-654 <MIN>
A;Cross-references: UNIPROT:Q19284; EMBL:U40958; PIDN:AAA81764.1; CESP:F09F9.4
C;Genetics:
A;Gene: CESP:F09F9.4
A;Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

Query Match 90.3%; Score 56; DB 2; Length 654;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	WSXWSXCSXXCG 12
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db
322 WSEWSACSETCG 333

RESULT 3

A48569
antigen Em100 - Eimeria maxima
C:/Species: Eimeria maxima
C:/Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:/Accession: A48569
R:/Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
A:/Title: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella mi
A:/Reference number: A48569; MUID:93149203; PMID:8426611
A:/Accession: A48569
A:/Status: preliminary
A:/Molecule type: nucleic acid
A:/Residues: 1-724 <PAS>
A:/Cross-references: UNIPROT:Q04588; GB:M99058; NID:G158890; PID:G158891
A:/Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIIP:123777)
F:/45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
F:/238-296/Domain: thrombospondin type 1 repeat homology <THR1>
F:/309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F:/372-432/Domain: thrombospondin type 1 repeat homology <THR3>
F:/433-493/Domain: thrombospondin type 1 repeat homology <THR4>
F:/494-556/Domain: thrombospondin type 1 repeat homology <THR5>
F:/550-610/Domain: thrombospondin type 1 repeat homology <THR6>

RESULT 4

T00326
 T00326
 hypothetical protein KIAA0550 - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 15-Mar-2004
 C:Accession: T00326
 R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
 DNA Res. 5, 31-39, 1998
 A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
 A:Reference number: Z14086; MUID:98290545; PMID:9628581
 A:Accession: T00326
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-984 <NAG>
 A:Cross-references: EMBL:AB011122; NID:G3043623; PIDN:BAA25476.1; PID:G3043624
 A:Experimental source: brain
 C:Genetics:
 A:Note: KIAA0550
 E:244-298/domain: thrombospondin type 1 repeat homology <THR3>

RESULT 5

Tl8856
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: Tl8856; T24653
 R:McMurray, A.

submitted to the EMBL Data Library, July 1995

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19031

A;Accession: T18856

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WIL>

A;Cross-references: UNIPROT:Q8MYA8; EMBL:Z50004; PIDN:CAA90293.1; GSPDB:GN00028; CESP:C02B4

A;Experimental source: clone C02B4

R;McMurray, A.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z19917

A;Accession: T24653

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1444 <WT2>

A;Cross-references: EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:C02B4.1

A;Experimental source: clone T07C5

C;Genetics:

A;Gene: CESP:C02B4.1

A;Map position: X

A;Introns: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 566/3

RESULT 6

T00028
brain-specific angiogenesis inhibitor 3 - human
N;Alternate names: BAI3 protein
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00028
R;Shiratsuchi, T.; Nishimori, H.; Ichise, H.; Nakamura, Y.; Tokino, T.
Cytogenet. Cell Genet. 79, 103-108, 1997
A;Title: Cloning and characterization of BAI2 and BAI3, novel genes homologous to BAI1
A;Reference number: Z14066; MUID:98194217; PMID:9533023
A;Accession: T00028
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1522 <SHI>
A;Cross-references: UNIPROT:O60242; EMBL:AB005299; NID:g3021700; PIDN:BAA25
A;Experimental source: brain
C;Genetics:
A;Gene: GDB:BAI3
A;Cross-references: GDB:9838090; OMIM:602684
A;Map position: 6q12-6q12
A;Map position: 6q12-6q12 repeat homology <THR3>

RESULTS

protein CTRP - malaria parasite (Plasmodium falciparum)
 C/Species: Plasmodium falciparum
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T18397
 R/Trottein, F.; Triglia, T.; Cowman, A.F.
 Mol. Biochem. Parasitol. 74, 129-142, 1995
 A/Title: Molecular cloning of a gene from Plasmodium falciparum that codes
 A/Reference number: Z18926; MUID:96360471; PMID:8719155

A;Cross-references: UNIPROT:Q22631; EMBL:Z68011; PIDN:CAA92014.1; GSPDB:GN00028; CESP:T21B6
A;Experimental source: clone T21B6
C;Genetics:
A;Gene: CESP:T21B6.3
A;Map position: X
A;Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2

R:Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A>Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A:Reference number: A47723; MUID:93376785; PMID:8367492

RESULT 10

C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A47379; A42173
R;LaBell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDNA: pote
A;Reference number: A47379; MUID:94010892; PMID:8406456
A;Accession: A47379
A;Molecule type: mRNA
A;Residues: 1-1172 <LA2>
A;Cross-references: UNIPROT:P35442; GB:L12350; NID:g307505; PIDN:AAA03703.1; PID:g307506
R;LaBell, T.L.; Milewicz, D.J.; Distèche, C.M.; Byers, P.H.
Genomics 12, 421-429, 1992
A;Title: Thrombospondin II: partial cDNA sequence, chromosome location, and expression c
A;Reference number: A42173; MUID:92217961; PMID:1559694
A;Accession: A42173
A;Molecule type: mRNA
A;Residues: 560-1172 <LA2>
A;Cross-references: GB:M81339
A;Experimental source: fibroblast
A;Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
C;Genetics:
A;Gene: GDB:THBS2; TSP2
A;Cross-references: GDB:128789; OMIM:188061
A;Map position: 6q27-6q27
C;Complex: homotrimer, disulfide linked
C;Function:
A;Description: participates in cell migration and adhesion, and in platelet aggregation
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vo
C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-1172/Product: thrombospondin 2 #status predicted <MAT>
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF1>
F;652-691/Domain: EGF homology <EGF>
F;928-930/Region: cell attachment (R-G-D) motif
F;151,316,330,457,584,710,1069/Binding site: carbohydrate (Asn) (covalent) #status predi
F;167-226/Disulfide bonds: #status predicted
F;266,270/Disulfide bonds: interchain #status predicted
F;612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 88.7%; Score 55; DB 1; Length 1172;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
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Db 443 WSPWSSCSVTCTG 454

RESULT 15
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thrombospondin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42587; A39851
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A;Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A;Reference number: A42587; MUID:92147683; PMID:1371115
A;Accession: A42587
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-1172 <LAH>
A;Cross-references: UNIPROT:Q03350; GB:L07803; GB:M87275; NID:g340421; PIDN:AAA53064.1;
A;Note: sequence extracted from NCBI backbone (NCBIP:81502)
R;Bornstein, P.; O'Rourke, K.; Wikstrom, K.; Wolf, F.W.; Katz, R.; Li, P.; Dixit, V.M.
J. Biol. Chem. 266, 12821-12824, 1991
A;Title: A second, expressed thrombospondin gene (Thbs2) exists in the mouse genome.
A;Reference number: A39851; MUID:91302287; PMID:1712771

A;Accession: A39851
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-873 <BOR>
A;Cross-references: GB:M64866; NID:g201994; PIDN:AAA40432.1; PID:g201995
C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vo
C;Keywords: calcium binding; glycoprotein
F;319-377/Domain: von Willebrand factor type C repeat homology <VWC>
F;380-431/Domain: thrombospondin type 1 repeat homology <THR1>
F;436-492/Domain: thrombospondin type 1 repeat homology <THR2>
F;493-549/Domain: thrombospondin type 1 repeat homology <THR3>
F;553-588/Domain: EGF homology <EGF1>
F;652-691/Domain: EGF homology <EGF>

Query Match 88.7%; Score 55; DB 2; Length 1172;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
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Db 443 WSPWSSCSVTCTG 454

Search completed: April 1, 2005, 14:00:30
Job time : 18.6957 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:59:39 ; Search time 61.8261 Seconds
(without alignments)
64.360 Million cell updates/sec

Title: US-09-462-909D-7
Perfect score: 62
Sequence: 1 WSXWSXCSXXCG 12

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Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	91.9	1077	15 US-10-190-115-43	Sequence 43, Appl
2	57	91.9	1077	15 US-10-369-072-43	Sequence 43, Appl
3	56	90.3	52	15 US-10-019-065A-21	Sequence 21, Appl
4	56	90.3	660	11 US-09-939-853A-96	Sequence 96, Appl
5	56	90.3	997	9 US-09-918-171A-7	Sequence 7, Appli
6	56	90.3	997	10 US-09-981-151A-32	Sequence 32, Appl
7	56	90.3	997	16 US-10-408-765A-1094	Sequence 1094, Ap
8	56	90.3	1255	15 US-10-312-352-23	Sequence 23, Appl
9	56	90.3	1522	14 US-10-225-567A-346	Sequence 346, App
10	56	90.3	1686	15 US-10-386-414-2	Sequence 2, Appli
11	56	90.3	1690	9 US-09-788-043C-5	Sequence 5, Appli
12	56	90.3	4123	14 US-10-213-509-5	Sequence 5, Appli
13	56	90.3	4219	15 US-10-085-198-2	Sequence 2, Appli

14	55	88.7	23	14	US-10-042-696-12	Sequence 12, Appl
15	55	88.7	41	15	US-10-074-978A-408	Sequence 408, App
16	55	88.7	42	15	US-10-074-978A-406	Sequence 406, App
17	55	88.7	53	15	US-10-019-065A-13	Sequence 13, Appl
18	55	88.7	53	15	US-10-019-065A-14	Sequence 14, Appl
19	55	88.7	55	15	US-10-019-065A-7	Sequence 7, Appli
20	55	88.7	55	15	US-10-019-065A-10	Sequence 10, Appl
21	55	88.7	55	17	US-10-883-144-41	Sequence 41, Appl
22	55	88.7	56	17	US-10-883-144-36	Sequence 36, Appl
23	55	88.7	57	9	US-09-802-094-5	Sequence 5, Appli
24	55	88.7	57	9	US-09-802-094-6	Sequence 6, Appli
25	55	88.7	57	10	US-09-373-658-7	Sequence 7, Appli
26	55	88.7	57	10	US-09-373-658-10	Sequence 10, Appl
27	55	88.7	57	11	US-09-989-687-7	Sequence 7, Appli
28	55	88.7	57	11	US-09-989-687-10	Sequence 10, Appl
29	55	88.7	58	16	US-10-296-733-21	Sequence 21, Appl
30	55	88.7	61	16	US-10-296-733-23	Sequence 23, Appl
31	55	88.7	63	16	US-10-296-733-22	Sequence 22, Appl
32	55	88.7	170	15	US-10-419-462-43	Sequence 43, Appl
33	55	88.7	170	16	US-10-296-733-20	Sequence 20, Appl
34	55	88.7	170	16	US-10-296-733-25	Sequence 25, Appl
35	55	88.7	170	16	US-10-296-733-27	Sequence 27, Appl
36	55	88.7	170	17	US-10-782-968-43	Sequence 43, Appl
37	55	88.7	185	9	US-09-867-550-1306	Sequence 1306, Ap
38	55	88.7	194	15	US-10-019-065A-32	Sequence 32, Appl
39	55	88.7	218	13	US-10-036-869-1	Sequence 1, Appli
40	55	88.7	242	9	US-09-919-603-5	Sequence 5, Appli
41	55	88.7	246	15	US-10-296-115-977	Sequence 977, App
42	55	88.7	300	9	US-09-919-603-7	Sequence 7, Appli
43	55	88.7	311	9	US-09-863-824-6	Sequence 6, Appli
44	55	88.7	349	15	US-10-161-493-126	Sequence 126, App
45	55	88.7	353	15	US-10-161-493-128	Sequence 128, App

ALIGNMENTS

RESULT 1

US-10-190-115-43
; Sequence 43, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01


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; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 43
; LENGTH: 1077
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-43

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Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 WSXWSXCSXXCG 12
Db      847 WSSWSKCSATCG 858

RESULT 2
US-10-369-072-43
; Sequence 43, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szerkeres, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
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; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586

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; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 1077
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-369-072-43

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Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 WSXWSXCSXXCG 12
Db      847 WSSWSKCSATCG 858

RESULT 3
US-10-019-065A-21
; Sequence 21, Application US/10019065A
; Publication No. US20040086501A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Corporation
; TITLE OF INVENTION: Protein Having Activity As An Angiogenesis Modulator
; FILE REFERENCE: MSB-7265-PCT
; CURRENT APPLICATION NUMBER: US/10/019,065A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/266,300
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated type 1 thrombospondin domain sequence
US-10-019-065A-21

Query Match          90.3%; Score 56; DB 15; Length 52;
Best Local Similarity 66.7%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 WSXWSXCSXXCG 12
Db      6 WSQWSTCSVTCG 17

RESULT 4
US-09-939-853A-96
; Sequence 96, Application US/09939853A
; Publication No. US20040039163A1
; GENERAL INFORMATION:
; APPLICANT: Burgess et al.
; TITLE OF INVENTION: No. US20040039163A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-099
; CURRENT APPLICATION NUMBER: US/09/939,853A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/267,300
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/269,961
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/277,337

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; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Cryptosporidium wrairi
US-09-939-853A-96

Query Match 90.3%; Score 56; DB 11; Length 660;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSCXXCG 12
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Db 352 WSEWSDCSTSCG 363

RESULT 5

US-09-918-171A-7
; Sequence 7, Application US/09918171A
; Patent No. US20020110894A1
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/04193
; CURRENT APPLICATION NUMBER: US/09/918,171A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/369,364
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-7
US-09-918-171A-7

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Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 6

US-09-981-151A-32
; Sequence 32, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glennnda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shinkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A

; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-32

Query Match 90.3%; Score 56; DB 10; Length 997;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSCXXCG 12
||| ||| |||
Db 544 WSAWSICSRSCG 555

RESULT 7

US-10-408-765A-1094
; Sequence 1094, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1094
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1094

Query Match 90.3%; Score 56; DB 16; Length 997;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 544 WSAWSICRSRSCG 555

RESULT 8
US-10-312-352-23
; Sequence 23, Application US/10312352
; Publication No. US20040053824A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: HE, Ann; BATRA, Sajeev
; APPLICANT: LO, Terence P.; NGUYEN, Dannie B.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam
; APPLICANT: BURFORD, Neil; YAO, Monique G.
; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
; APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
; APPLICANT: LU, Yan; BOROWSKY, Mark L.
; APPLICANT: LU, Dying Aina M.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Junming; GURURAJAN, Rajagopal
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
; APPLICANT: XU, Yuming; KALLICK, Deborah A.
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
; APPLICANT: DELEGEANE, Angelo M.; LEE, Sally
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PF-0794 USN
; CURRENT APPLICATION NUMBER: US/10/312,352
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/US01/21067
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,454
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/219,462
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 60/240,111
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/240,106
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/244,021
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/248,887
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/249,570
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 23
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053824A1 55022490CD1
US-10-312-352-23

Query Match 90.3%; Score 56; DB 15; Length 1255;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 113 WSAWSICRSRSCG 124

RESULT 9
US-10-225-567A-346
; Sequence 346, Application US/10225567A

; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 1522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-346

Query Match 90.3%; Score 56; DB 14; Length 1522;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 297 WSQWSTCSVTGCG 308

RESULT 10
US-10-386-414-2
; Sequence 2, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; FILE REFERENCE: MPI03-0210MNIM
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1686
; TYPE: PRT

; ORGANISM: Homo Sapien
US-10-386-414-2

Query Match 90.3%; Score 56; DB 15; Length 1686;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 544 WSAWSICSRSCG 555

RESULT 11

US-09-788-043C-5
; Sequence 5, Application US/09788043C
; Patent No. US20020107361A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Renu
; APPLICANT: Zuo, Fengrong
; APPLICANT: Klönowski, Paul
; TITLE OF INVENTION: No. US20020107361A1el Metalloproteases Having
; TITLE OF INVENTION: Thrombospondin Domains and Nucleic Acid Compositions
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: ROCH-004
; CURRENT APPLICATION NUMBER: US/09/788,043C
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/184,152
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1690
; TYPE: PRT
; ORGANISM: human
US-09-788-043C-5

Query Match 90.3%; Score 56; DB 9; Length 1690;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 548 WSAWSICSRSCG 559

RESULT 12

US-10-213-509-5
; Sequence 5, Application US/10213509
; Publication No. US20030054485A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Joseph
; APPLICANT: Scott, Matthew
; TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
; FILE REFERENCE: STAN-232
; CURRENT APPLICATION NUMBER: US/10/213,509
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/311,720
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4123
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-213-509-5

Query Match 90.3%; Score 56; DB 14; Length 4123;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 2518 WSVWSSCSRSCG 2529

RESULT 13

US-10-085-198-2
; Sequence 2, Application US/10085198
; Publication No. US2004000907A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-2

Query Match 90.3%; Score 56; DB 15; Length 4219;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| ||| |||
Db 2614 WSVWSSCSRSCG 2625

RESULT 14

US-10-042-696-12
; Sequence 12, Application US/10042696
; Publication No. US20030171298A1
; GENERAL INFORMATION:
; APPLICANT: Tuszyński, George
; APPLICANT: Williams, Taify
; APPLICANT: Actor, Paul
; TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT THROMBOSPONDIN ACT
; FILE REFERENCE: 07206-0021
; CURRENT APPLICATION NUMBER: US/10/042,696
; CURRENT FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 12
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic fragment/analog of
; OTHER INFORMATION: thrombospondin
US-10-042-696-12

Fri Apr 1 15:03:04 2005

Query Match 88.7%; Score 55; DB 14; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 4 WSPWSSCSVTTCG 15

RESULT 15

US-10-074-978A-408
; Sequence 408, Application US/10074978A
; Publication No. US20040010119A1

GENERAL INFORMATION:

; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A11le
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 408
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-408

Query Match 88.7%; Score 55; DB 15; Length 41;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 3 WSLWSVCSVTTCG 14

Search completed: April 1, 2005, 14:22:17
Job time : 63.8261 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:44:22 ; Search time 21.1304 Seconds
(without alignments)
42.393 Million cell updates/sec

Title: US-09-462-909D-7
Perfect score: 62
Sequence: 1 WSXWSXCSXXCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	90.3	479	4	US-09-270-767-46823
2	56	90.3	677	4	US-09-270-767-58094
3	56	90.3	847	4	US-09-270-767-42783
4	56	90.3	997	3	US-09-369-364A-7
5	55	88.7	23	1	US-07-646-531D-6
6	55	88.7	23	2	US-08-488-273-6
7	55	88.7	23	3	US-09-197-770B-12
8	55	88.7	23	6	5426100-6
9	55	88.7	23	6	5426100-6
10	55	88.7	51	2	US-08-799-173A-11
11	55	88.7	51	4	US-09-170-042A-11
12	55	88.7	60	1	US-07-646-531D-12
13	55	88.7	60	2	US-08-488-273-12
14	55	88.7	60	6	5426100-12
15	55	88.7	60	6	5426100-12
16	55	88.7	218	3	US-08-985-526-1
17	55	88.7	239	5	PCT-US93-01652-1
18	55	88.7	441	3	US-08-985-526-3
19	55	88.7	568	1	US-07-862-021B-14
20	55	88.7	568	5	PCT-US93-03164-14
21	55	88.7	787	4	US-09-825-294-207
22	55	88.7	787	4	US-09-970-966-207
23	55	88.7	788	2	US-08-918-914-4
24	55	88.7	802	1	US-07-862-021B-12
25	55	88.7	802	1	US-08-313-288B-12
26	55	88.7	802	5	PCT-US93-03164-12
27	55	88.7	807	1	US-07-862-021B-10

28	55	88.7	807	1	US-08-313-288B-10	Sequence 10, Appl
29	55	88.7	807	4	US-09-132-769-1	Sequence 1, Appli
30	55	88.7	807	4	US-09-132-769-3	Sequence 3, Appli
31	55	88.7	807	4	US-09-132-769-5	Sequence 5, Appli
32	55	88.7	807	4	US-09-640-173-186	Sequence 186, App
33	55	88.7	807	4	US-09-713-550-186	Sequence 186, App
34	55	88.7	807	4	US-09-825-294-186	Sequence 186, App
35	55	88.7	807	4	US-09-970-966-186	Sequence 186, App
36	55	88.7	807	5	PCT-US93-03164-10	Sequence 10, Appl
37	55	88.7	1045	4	US-09-949-016-1112	Sequence 1112, A
38	55	88.7	1170	4	US-08-313-288B-20	Sequence 20, Appl
39	55	88.7	1170	4	US-09-657-472-2	Sequence 2, Appli
40	55	88.7	1172	1	US-08-313-288B-19	Sequence 19, Appl
41	55	88.7	1172	4	US-09-949-016-6333	Sequence 6333, Ap
42	55	88.7	1184	2	US-08-918-914-1	Sequence 1, Appli
43	55	88.7	1184	3	US-08-996-083-3	Sequence 3, Appli
44	55	88.7	1224	4	US-09-930-872-4	Sequence 4, Appli
45	55	88.7	1224	4	US-10-217-774-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-270-767-46823
; Sequence 46823, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46823
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46823

Query Match 90.3%; Score 56; DB 4; Length 479;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
DB 242 WSEWSACSVTCG 253

RESULT 2
US-09-270-767-58094
; Sequence 58094, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58094
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58094

Query Match 90.3%; Score 56; DB 4; Length 677;
Best Local Similarity 66.7%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12

ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-2U4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-273-6

Query Match 88.7%; Score 55; DB 2; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 4 WSPWSSCSVTG 15

RESULT 7
US-09-197-770B-12
Sequence 12, Application US/09197770B
Patent No. 6339062
GENERAL INFORMATION:
APPLICANT: Tuszyński, George
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR INHIBIT
TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
FILE REFERENCE: 07206-0021
CURRENT APPLICATION NUMBER: US/09/197,770B
CURRENT FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 12
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: fragment/ analog of thrombospondin
US-09-197-770B-12

Query Match 88.7%; Score 55; DB 3; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 4 WSPWSSCSVTG 15

RESULT 8
5426100-6
Patent No. 5426100
APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
THROMBOSPONDIN
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,146
FILING DATE: 20-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 896,527
FILING DATE: 09-JUN-1992
APPLICATION NUMBER: 483,527

FILING DATE: 22-FEB-1990
SEQ ID NO: 6:
LENGTH: 23
5426100-6

Query Match 88.7%; Score 55; DB 6; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 4 WSPWSSCSVTG 15

RESULT 9
5426100-6
Patent No. 5426100
APPLICANT: DEUTCH, ALAN H.; TUSZYNSKI, GEORGE
TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
THROMBOSPONDIN
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,146
FILING DATE: 20-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 896,527
FILING DATE: 09-JUN-1992
APPLICATION NUMBER: 483,527
FILING DATE: 22-FEB-1990
SEQ ID NO: 6:
LENGTH: 23
5426100-6

Query Match 88.7%; Score 55; DB 6; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 4 WSPWSSCSVTG 15

RESULT 10
US-08-799-173A-11
Sequence 11, Application US/08799173A
Patent No. 5871969
GENERAL INFORMATION:
APPLICANT: HASTINGS, GREGG,
APPLICANT: PATRICK J. DILLON
TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,173A
FILING DATE: 11-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504

```
;
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-799-173A-11
;
; Query Match      88.7%; Score 55; DB 2; Length 51;
; Best Local Similarity 66.7%; Pred. No. 0.46;
; Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY      1 WSXWSXCSXXCG 12
      |||||
Db      6 WSEWSDCSVTCG 17
;
; RESULT 11
; US-09-170-042A-11
; Sequence 11, Application US/09170042A
; Patent No. 6759512
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg
; APPLICANT: Dillon, Patrick
; TITLE OF INVENTION: Human Neuronal Attachment Factor-1
; FILE REFERENCE: PF226D1
; CURRENT APPLICATION NUMBER: US/09/170,042A
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 51
; TYPE: PRT
; ORGANISM: rat
; US-09-170-042A-11
;
; Query Match      88.7%; Score 55; DB 4; Length 51;
; Best Local Similarity 66.7%; Pred. No. 0.46;
; Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY      1 WSXWSXCSXXCG 12
      |||||
Db      6 WSEWSDCSVTCG 17
;
; RESULT 12
; US-07-646-531D-12
; Sequence 12, Application US/07646531D
; Patent No. 5200397
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan Howard
; APPLICANT: Tuszyński, George Paul
; TITLE OF INVENTION: Peptide Fragments and Analogs of
; TITLE OF INVENTION: Peptide Fragments and Analogs of
; TITLE OF INVENTION: Thrombospondin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. R. Grace & Co.-Conn.
; STREET: 7379 Route 32
; CITY: Columbia
; STATE: Maryland
; COUNTRY: USA
; ZIP: 21044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,531D
; FILING DATE: 19910131
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Appleby, Vanessa L.
; REGISTRATION NUMBER: 33223
; REFERENCE/DOCKET NUMBER: 01-7896
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 531-4515
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-646-531D-12
;
; Query Match      88.7%; Score 55; DB 1; Length 60;
; Best Local Similarity 66.7%; Pred. No. 0.52;
; Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
QY      1 WSXWSXCSXXCG 12
      |||||
Db      7 WSPWSSCSVTCG 18
;
; RESULT 13
; US-08-488-273-12
; Sequence 12, Application US/08488273
; Patent No. 5840692
; GENERAL INFORMATION:
; APPLICANT: Deutch, Alan H.
; APPLICANT: Tuszyński, George P.
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
; TITLE OF INVENTION: THROMBOSPONDIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,273
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/359,263
; FILING DATE: 19-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,527
; FILING DATE: 09-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/483,527
; FILING DATE: 22-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-2U4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; STRANDEDNESS:
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-273-12

Query Match      88.7%; Score 55; DB 2; Length 60;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 WSXWSXCSXXCG 12
Db      7 WSPWSSCSVTCG 18

RESULT 14
5426100-12
;Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.;TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
;.. THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
;SEQ ID NO:12:
; LENGTH: 60
5426100-12

Query Match      88.7%; Score 55; DB 6; Length 60;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 WSXWSXCSXXCG 12
Db      7 WSPWSSCSVTCG 18

RESULT 15
5426100-12
;Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.;TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PEPTIDE FRAGMENTS AND ANALOGS OF
;.. THROMBOSPONDIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,146
; FILING DATE: 20-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 896,527
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 483,527
; FILING DATE: 22-FEB-1990
;SEQ ID NO:12:
; LENGTH: 60
5426100-12

Query Match      88.7%; Score 55; DB 6; Length 60;
Best Local Similarity 66.7%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 WSXWSXCSXXCG 12
Db      7 WSPWSSCSVTCG 18

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 13:22:55 ; Search time 83.7391 Seconds
(without alignments)
55.424 Million cell updates/sec

Title: US-09-462-909D-7
Perfect score: 62
Sequence: 1 WSXWSXCSXXCG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseg_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	91.9	324	8 ADP04871	Adp04871 Sea squir
2	56	90.3	12	2 AAW97445	Aaw97445 Peptide t
3	56	90.3	27	4 AAE04264	Aae04264 Human gen
4	56	90.3	100	4 AAE04262	Aae04262 Human gen
5	56	90.3	149	4 AAE04263	Aae04263 Human gen
6	56	90.3	189	4 AAE04268	Aae04268 Human gen
7	56	90.3	191	4 AAE04266	Aae04266 Human gen
8	56	90.3	206	3 AAB08135	Aab08135 Amino aci
9	56	90.3	763	4 ABB62815	Abb62815 Drosophil
10	56	90.3	997	4 AAB72283	Aab72283 Human ADA
11	56	90.3	997	7 ADJ69288	Adj69288 Human hea
12	56	90.3	1083	4 ABB61710	Abb61710 Drosophil
13	56	90.3	1255	5 ADI28031	Adi28031 ECMCAD pr
14	56	90.3	1515	8 ADO29008	Ado29008 Mouse nov
15	56	90.3	1522	2 AAW99302	Aaw99302 Human BAI
16	56	90.3	1522	3 AAB23601	Aab23601 Human sec
17	56	90.3	1522	6 ABP81930	Abp81930 Human bra
18	56	90.3	1522	8 ADO29007	Ado29007 Human nov
19	56	90.3	1682	4 ABB66442	Abb66442 Drosophil
20	56	90.3	1686	4 AAE00934	Aae00934 Human 278
21	56	90.3	1686	4 AAE00913	Aae00913 Human 278
22	56	90.3	1686	4 AAB74944	Aab74944 Human ADA
23	56	90.3	1686	8 ADJ58902	Adj58902 Human ADA
24	56	90.3	1690	4 AAB86949	Aab86949 Human met
25	56	90.3	1784	3 AAB41379	Aab41379 Human ORF

26	56	90.3	4123	7 ABU62079	Abu62079 Human jel
27	56	90.3	4219	5 ADH48718	Adh48718 NOVI prot
28	56	90.3	4561	4 ABG30203	Abg30203 Novel hum
29	56	90.3	5737	7 ADN95228	Adn95228 Human BEC
30	56	90.3	9222	4 ABG21064	Abg21064 Novel hum
31	55	88.7	23	2 AAR13630	Aar13630 Thrombos
32	55	88.7	23	2 AAW81483	Aaw81483 Thrombos
33	55	88.7	23	5 AAE20782	Aae20782 Alternati
34	55	88.7	23	8 ADM80538	Adm80538 Thrombos
35	55	88.7	50	7 ADD44504	Add44504 Polypepti
36	55	88.7	51	2 AAW92465	Aaw92465 Rat F-spo
37	55	88.7	51	8 ADQ94995	Adq94995 Rat F-spo
38	55	88.7	51	8 ADR03574	Adr03574 Rat F-spo
39	55	88.7	57	2 AAY49504	Aay49504 Human MET
40	55	88.7	57	2 AAY49507	Aay49507 Human MET
41	55	88.7	57	4 AAG79062	Aag79062 Biologica
42	55	88.7	57	4 AAG79061	Aag79061 Biologica
43	55	88.7	57	4 AAB50006	Aab50006 TSP1 doma
44	55	88.7	57	4 AAB50009	Aab50009 TSP2 doma
45	55	88.7	60	2 AAR13641	Aar13641 Thrombos

ALIGNMENTS

RESULT 1

ADP04871	ID	ADP04871	standard; protein; 324 AA.
XX	AC	ADP04871;	
XX	DT	29-JUL-2004	(first entry)
XX	DB	Sea squirt protein with tissue specific expression in development Seq466.	
XX	KW	sea squirt; regeneration medicine; gene therapy; cell proliferation;	
XX	KW	differentiation; reproduction; environmental measurement; water survey.	
XX	OS	Ciona intestinalis.	
XX	PN	JP2004057129-A.	
XX	PD	26-FEB-2004.	
XX	PF	31-JUL-2002; 2002JP-00222593.	
XX	PR	31-JUL-2002; 2002JP-00222593.	
XX	PA	(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.	
XX	DR	WPI; 2004-287079/27.	
XX	XX	N-PSDB; ADP04870.	
PT	PT	Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.	
XX	PS	Claim 1; SEQ ID NO 466; 1846pp; Japanese.	
XX	CC	This invention relates to novel genes and the encoded proteins thereof that are derived from the sea squirt Ciona intestinalis. Specifically, it refers to those genes that are expressed in the tissues or organs of the sea squirt during its developmental phase. The present invention describes the identification of these genes as useful for elucidation of the mechanism of development and hence for developing regeneration medicines and gene therapy techniques. Accordingly, they can be used in the research of various genetic diseases, as well as the analysis of cell proliferation, differentiation and reproduction. Furthermore, such compositions can be useful for environmental measurements and water surveys, particularly for sea water surveys, and also for the preparation of transformed sea squirt for improving edibility of sea squirt such as Halocynthia roretzi. This polypeptide sequence is a sea squirt protein sequence that has tissue specific expression during development, given in	

Fri Apr 1 15:03:04 2005

CC an exemplification of the invention.

XX

SQ Sequence 324 AA;

Query Match 91.9%; Score 57; DB 8; Length 324;

Best Local Similarity 66.7%; Pred. No. 2.9;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WSXWSXCSXXCG 12

Db 85 WSSWSRCSSSCG 96

RESULT 2

AAW97445

ID AAW97445 standard; peptide; 12 AA.

XX

AC AAW97445;

XX

DT 19-MAY-1999 (first entry)

XX

DE Peptide that is useful for regenerating the nervous system.

XX

KW Neuronal sprouting; cerebral cortex; spinal cord cell; aggregation;

KW neurite defasciculation; regeneration; nervous system cell;

KW neurodegeneration; Alzheimer's; Parkinson's disease; multiple sclerosis;

KW myopathy; synapse formation; neuroblastoma.

XX

OS Synthetic.

XX

PN WO9903890-A1.

XX

PD 28-JAN-1999.

XX

PF 16-JUL-1998; 98WO-FR001556.

XX

PR 16-JUL-1997; 97FR-00009016.

XX

PA (UYAU-) UNIV AUVERGNE.

XX

PI Meinie A, Monnerie H, Gobron S;

XX

DR WPI; 1999-132166/11.

XX

XX New polypeptides for promoting growth of neurons - useful for treatment of neurodegeneration, neuroblastoma and as additives for neuronal cell cultures.

PT

PT Claim 6; Page 14; 29pp; French.

XX

PS The present sequence represents a peptide that stimulates neuronal (particularly axonal) sprouting in neurons of the cerebral cortex, and in spinal cord cells inhibits aggregation and defasciculation of neurites while increasing formation of synaptic contacts. The peptide is used to regenerate nervous system cells, particularly for treating neurodegeneration (e.g. Alzheimer's or Parkinson's diseases, multiple sclerosis and myopathy), other conditions requiring regeneration (particularly elongation and synapse formation) or neuroblastoma. The peptide can also be used as an additive for neuronal cell cultures

XX

SQ Sequence 12 AA;

Query Match 90.3%; Score 56; DB 2; Length 12;

Best Local Similarity 66.7%; Pred. No. 0.25;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WSXWSXCSXXCG 12

Db 1 WSGWSSCSRSCG 12

RESULT 3

AAE04264

ID AAE04264 standard; peptide; 27 AA.

XX

AC AAE04264;

XX

DT 09-AUG-2001 (first entry)

XX

DE Human gene 8 encoded secreted protein fragment, SEQ ID NO:127.

XX

KW Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnery; cell culture; chemotaxis; food additive; binding partner identification; chromosome 7.

XX

OS Homo sapiens.

XX

PN WO200136432-A2.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-US031162.

XX

PR 19-NOV-1999; 99US-0166415P.

XX

PR 30-JUN-2000; 2000US-0215136P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Komatsoulis GA, Baker KP, Young PE;

XX

DR WPI; 2001-343793/36.

XX

XX Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

PT

PT Disclosure; Page 32; 509pp; English.

XX

PS AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, allergies, diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infectious proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention

XX

SQ Sequence 27 AA;

Query Match 90.3%; Score 56; DB 4; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSCXXCG 12
DB 13 WSAWSSCSAPCG 24

RESULT 4
AAE04262
ID AAE04262 standard; protein; 100 AA.
AC AAE04262;
DT 09-AUG-2001 (first entry)
XX Human gene 8 encoded secreted protein fragment, SEQ ID NO:124.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW endocrine disorder; infection; wound healing; vulnery; cell culture;
KW chemotaxis; food additive; binding partner identification; chromosome 7.
OS Homo sapiens.
XX
XX WO200136432-A2.
XX
XX 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-US031162.
XX
XX 19-NOV-1999; 99US-0166415P.
XX
XX 30-JUN-2000; 2000US-0215136P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;
XX WPI; 2001-343793/36.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
XX Disclosure; Page 493; 509pp; English.
XX
XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
XX protein genes, and AAE04199-AAE04239 represent the proteins they encode.
XX AAE04240-AAE04297 represent human secreted protein fragments or variants.
XX The secreted proteins and their genes are useful for preventing, treating
XX or ameliorating medical conditions, e.g., by protein or gene therapy.
XX Pathological conditions can be diagnosed by determining the amount of the
XX new protein in a sample or by determining the presence of mutations in
XX based on the tissues in which they are most highly expressed, and include
XX developing products for the diagnosis or treatment of proliferative
XX disorders, cancer, tumours, foetal and developmental abnormalities,
XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,
XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
XX angiogenic disorders, kidney disorders, gastrointestinal disorders,
XX pregnancy-related disorders, endocrine disorders, and infections. The
XX proteins can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin ageing due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,

CC to regenerate tissues, to identify their cognate ligands or binding
CC partners, and in chemotaxis, and can be used as a food additive or
CC preservative to modify storage properties. Antibodies specific for a
CC protein of the invention can be used in alleviating symptoms associated
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
CC present sequence represents a human secreted protein fragment referred to
CC in the disclosure of the invention
XX
SQ Sequence 100 AA;
Query Match 90.3%; Score 56; DB 4; Length 100;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSCXXCG 12
DB 11 WSAWSSCSAPCG 22

RESULT 5
AAE04263
ID AAE04263 standard; protein; 149 AA.
XX
AC AAE04263;
DT 09-AUG-2001 (first entry)
XX
XX Human gene 8 encoded secreted protein fragment, SEQ ID NO:126.
DE
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW endocrine disorder; infection; wound healing; vulnery; cell culture;
KW chemotaxis; food additive; binding partner identification; chromosome 7.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 115
FT /label= Unknown
FT /note= "Xaa equals any of the naturally occurring L-amino
FT acids"
FT Misc-difference 117
FT /label= Unknown
FT /note= "Xaa equals any of the naturally occurring L-amino
FT acids"
FT Misc-difference 121
FT /label= Unknown
FT /note= "Xaa equals any of the naturally occurring L-amino
FT acids"
FT Misc-difference 126
FT /label= Unknown
FT /note= "Xaa equals any of the naturally occurring L-amino
FT acids"
XX
PN WO200136432-A2.
XX
PD 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-US031162.
XX
XX 19-NOV-1999; 99US-0166415P.
XX
XX 30-JUN-2000; 2000US-0215136P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;

XX WPI; 2001-343793/36.

XX Isolated nucleic acid molecule encoding a human secreted protein is used

XX in preventing, treating or ameliorating a medical condition.

PT Disclosure; Page 494-495; 509pp; English.

XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted

XX protein genes, and AAE04199-AAE04239 represent the proteins they encode.

CC AAE04240-AAE04297 represent human secreted protein fragments or variants.

CC The secreted proteins and their genes are useful for preventing, treating

CC or ameliorating medical conditions, e.g., by protein or gene therapy.

CC Pathological conditions can be diagnosed by determining the amount of the

CC new protein in a sample or by determining the presence of mutations in

CC the new genes. Specific uses are described for each of the 18 genes,

CC based on the tissues in which they are most highly expressed, and include

CC developing products for the diagnosis or treatment of proliferative

CC disorders, cancer, tumours, foetal and developmental abnormalities,

CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune

CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,

CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),

CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,

CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,

CC angiogenic disorders, kidney disorders, gastrointestinal disorders, the

CC pregnancy-related disorders, endocrine disorders, and infections. The

CC proteins can also be used to aid wound healing and epithelial cell

CC proliferation, to prevent skin ageing due to sunburn, to maintain organs

CC before transplantation, for supporting cell culture of primary tissues,

CC to regenerate tissues, to identify their cognate ligands or binding

CC partners, and in chemotaxis, and can be used as a food additive or

CC preservative to modify storage properties. Antibodies specific for a

CC protein of the invention can be used in alleviating symptoms associated

CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,

CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The

CC present sequence represents a human secreted protein fragment referred to

CC in the disclosure of the invention

XX SQ Sequence 149 AA;

Query Match 90.3%; Score 56; DB 4; Length 149;

Best Local Similarity 66.7%; Pred. No. 2.1;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCXSCG 12

||| ||| |||

Db 1 WSAWSSCSAPCG 12

RESULT 6

AAE04268

ID AAE04268 standard; protein; 189 AA.

XX AAE04268;

XX 09-AUG-2001 (first entry)

XX Human gene 8 encoded secreted protein fragment, SEQ ID NO:131.

XX Human; secreted protein; proliferative disorder; cancer; tumour;

KW foetal abnormality; developmental abnormality; haematopoietic disorder;

KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

KW inflammation; allergy; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;

KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;

KW cardiovascular disorder; angiogenic disorder; kidney disorder;

KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;

KW endocrine disorder; infection; wound healing; vulnery; cell culture;

KW chemotaxis; food additive; binding partner identification; chromosome 7.

XX Homo sapiens.

OS WO200136432-A2.

XX PN

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-US031162.

XX 19-NOV-1999; 99US-0166415P.

XX 30-JUN-2000; 2000US-0215136P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;

XX WPI; 2001-343793/36.

XX Isolated nucleic acid molecule encoding a human secreted protein is used

XX in preventing, treating or ameliorating a medical condition.

XX Disclosure; Page 33; 509pp; English.

XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted

XX protein genes, and AAE04199-AAE04239 represent the proteins they encode.

XX AAE04240-AAE04297 represent human secreted protein fragments or variants.

XX The secreted proteins and their genes are useful for preventing, treating

XX or ameliorating medical conditions, e.g., by protein or gene therapy.

XX Pathological conditions can be diagnosed by determining the amount of the

XX new protein in a sample or by determining the presence of mutations in

XX the new genes. Specific uses are described for each of the 18 genes,

XX based on the tissues in which they are most highly expressed, and include

XX developing products for the diagnosis or treatment of proliferative

XX disorders, cancer, tumours, foetal and developmental abnormalities,

XX haematopoietic disorders, diseases of the immune system, AIDS, autoimmune

XX diseases (e.g., rheumatoid arthritis), inflammation, allergies,

XX neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),

XX cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,

XX psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,

XX angiogenic disorders, kidney disorders, gastrointestinal disorders, the

XX pregnancy-related disorders, endocrine disorders, and infections. The

XX proteins can also be used to aid wound healing and epithelial cell

XX proliferation, to prevent skin ageing due to sunburn, to maintain organs

XX before transplantation, for supporting cell culture of primary tissues,

XX to regenerate tissues, to identify their cognate ligands or binding

XX partners, and in chemotaxis, and can be used as a food additive or

XX preservative to modify storage properties. Antibodies specific for a

XX protein of the invention can be used in alleviating symptoms associated

XX with the disorders mentioned above, and in diagnostic immunoassays e.g.,

XX radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The

XX present sequence represents a human secreted protein fragment referred to

XX in the disclosure of the invention

XX SQ Sequence 189 AA;

Query Match 90.3%; Score 56; DB 4; Length 189;

Best Local Similarity 66.7%; Pred. No. 2.5;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCXSCG 12

||| ||| |||

Db 11 WSAWSSCSAPCG 22

RESULT 7

AAE04266

ID AAE04266 standard; protein; 191 AA.

XX AAE04266;

XX 09-AUG-2001 (first entry)

XX Human gene 8 encoded secreted protein fragment, SEQ ID NO:129.

XX Human; secreted protein; proliferative disorder; cancer; tumour;

KW foetal abnormality; developmental abnormality; haematopoietic disorder;

KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnery; cell culture; chemotaxis; food additive; binding partner identification; chromosome 7.

Homo sapiens.

WO200136432-A2.

25-MAY-2001.

15-NOV-2000; 2000WO-US031162.

19-NOV-1999; 99US-0166415P.

30-JUN-2000; 2000US-0215136P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Komatsoulis GA, Baker KP, Young PE; WPI; 2001-343793/36.

Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

Disclosure; Page 32; 509pp; English.

AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAE04199-AAE04239 represent the proteins they encode. AAE04240-AAE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention

Sequence 191 AA;

AA08135	standard; protein; 206 AA.
AA08135	
04-DEC-2000	(first entry)
Amino acid sequence of a KIAA0550 polypeptide.	
Type 1 repeat; thrombospondin-1; TSP-1; Type I repeat peptide; TRP; KIAA0688; KIAA0550; angiogenesis inhibitory protein; angiogenesis; cancer; tumour; rheumatoid arthritis; psoriasis; retinopathy; ocular angiogenic disease; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; haemophiliac joint; plaque neovascularisation; telangiectasia; angiofibroma; wound granulation; coronary collateral; cerebral collateral; arteriovenous malformation; ischemic limb angiogenesis; neovascular glaucoma; retrolental fibroplasia; fracture; vasculogenesis; heliobacter related disease; hematopoiesis; ovulation; menstruation; placental; birth control; embryo implantation.	
Homo sapiens.	
WO200047622-A2.	
17-AUG-2000.	
15-FEB-2000; 2000WO-GB000520.	
15-FEB-1999; 99GB-00003408.	
(OXFO-) OXFORD BIOMEDICA UK LTD.	
Mazarakis N, Martin-Rendon E, Kingsman SM;	
WPI; 2000-549137/50.	
Non-naturally occurring Type I repeat peptide (TRP) derived from human thrombospondin-1, KIAA0688 or KIAA0550 proteins, useful in the treatment of angiogenesis and/or cancer.	
Claim 5; Fig 7; 84pp; English.	
The present sequence represents a KIAA0550 polypeptide. The specification describes a non-naturally occurring Type I repeat peptide (TRP), derived from human thrombospondin-1 (hTSP-1), KIAA0688 or KIAA0550 proteins. The TRP protein is an angiogenesis inhibitory protein. TRP proteins are used for the treatment of conditions associated with angiogenesis and cancer. Angiogenic mediated diseases include tumours, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis), Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, neovascular glaucoma, retrolental fibroplasia, heliobacter related diseases, fractures, vasculogenesis, hematopoiesis, ovulation, menstruation and placental. TRPs are also useful in the treatment of disease of excessive or abnormal stimulation of endothelial cells. TRP can also be used as a birth control agent, as it prevents the vascularisation required for embryo implantation	
Sequence 206 AA;	

RESULT 9
ABB62815
ID ABB62815 standard; protein; 763 AA.
XX
XX ABB62815;
AC
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster polypeptide SEQ ID NO 15237.
DE
XX Drosophila melanogaster polypeptide; cell signalling; insecticide;
KW
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US009231.
PF
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL06918.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
PT
XX Disclosure; SEQ ID NO 15237; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 763 AA;
Query Match 90.3%; Score 56; DB 4; Length 763;
Best Local Similarity 66.7%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSXWSXCSXXCG 12
Db 520 WSVWSECSASCG 531
RESULT 10
AAB72283
ID AAB72283 standard; protein; 997 AA.
XX
XX AAB72283;
AC
XX 14-MAY-2001 (first entry)
DT
XX Human ADAMTS-7 amino acid sequence.
DE
XX ADAMTS-N; disintegrin; metalloprotease; thrombospondin type I motif;
KW tumour cachexia; inflammation; dermatosparaxis; EDS-VIIC; angiogenesis;
KW Ehlers-Danlos syndrome type VIIC; articular cartilage erosion; human;
KW metastasis; embryogenesis; egg implantation; chromosome 15; ADAMTS-7.
XX

XX Homo sapiens.
OS
XX WO200111074-A2.
PN
XX 15-FEB-2001.
PD
XX 03-AUG-2000; 2000WO-US021223.
PF
XX 06-AUG-1999; 99US-00369364.
PR
XX (CLEV-) CLEVELAND CLINIC FOUND.
PA (APTE/) APTE S S.
PA (HURS/) HURSKAINEN T L.
PA (HIRO/) HIROHATA S.
XX
XX Apte SS, Hurskainen TL, Hirohata S;
PI
XX WPI; 2001-159978/16.
XX
XX N-PSDB; AAF63440.
DR
XX Murine and human 'A Disintegrin-like And Metalloprotease domain with
PT Thrombospondin type I motifs' proteins and the nucleic acids encoding
PT them, useful for treating e.g. tumors, inflammation and arthritis.
XX
XX Claim 15; Fig 4; 181pp; English.
PS
XX This invention relates to murine and human ADAMTS-N (A disintegrin-like
CC and metalloprotease domain with thrombospondin type I motifs) proteins,
CC designated ADAMTS-5, 6, 7, 8, 9, 10 and R1. Also included in the
CC invention are cDNA sequences encoding the proteins, and antibodies
CC specific for the proteins. The nucleic acid sequences and proteins may be
CC used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate ADAMTS-N expression. Disorders that may be treated
CC using the nucleic acids, proteins and antibodies include, for example
CC tumour cachexia, inflammation, dermatosparaxis in cattle or Ehlers-Danlos
CC syndrome type VIIC (EDS-VIIC) in humans, erosion of articular cartilage
CC in arthritic (both inflammatory and non-inflammatory) disease,
CC angiogenesis, tumour growth and metastases, and they may also be used for
CC controlling embryogenesis and implantation of fertilised eggs. The
CC present sequence represents human ADAMTS-7. The human ADAMTS-7 gene is
CC located on chromosome 15
XX
SQ Sequence 997 AA;
Query Match 90.3%; Score 56; DB 4; Length 997;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 WSXWSXCSXXCG 12
Db 544 WSAWSICSRSCG 555
RESULT 11
ADJ69288
ID ADJ69288 standard; protein; 997 AA.
XX
XX ADJ69288;
AC
XX 06-MAY-2004 (first entry)
DT
XX Human heat mitochondrial protein as a therapeutic target SeqID1094.
DE
XX mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
XX Homo sapiens.
OS

XX WO2003087768-A2.
PN
XX
XX 23-OCT-2003.
PD
XX
XX
XX 04-APR-2003; 2003WO-US010870.
PF
XX
XX 12-APR-2002; 2002US-0372843P.
PR
XX 17-JUN-2002; 2002US-0389987P.
PR
XX 20-SEP-2002; 2002US-0412418P.
XX
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Faby ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
PI
XX WPI; 2003-845369/78.
DR
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 1094; 180pp; English.
PS
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cyostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
XX Sequence 997 AA;
SQ

Query Match 90.3%; Score 56; DB 7; Length 997;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 544 WSAWSICSRSCG 555

RESULT 12
ABB61710
ID ABB61710 standard; protein; 1083 AA.
XX
AC ABB61710;
XX
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster polypeptide SEQ ID NO 11922.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
XX WO200171042-A2.
PN
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US009231.
PF

XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR N-PSDB; ABL05813.
DR
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
PT
XX Disclosure; SEQ ID NO 11922; 21pp + Sequence Listing; English.
PS
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1083 AA;
SQ

Query Match 90.3%; Score 56; DB 4; Length 1083;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
Db 846 WSEWSACSVTCG 857

RESULT 13
ADI28031
ID ADI28031 standard; protein; 1255 AA.
XX
AC ADI28031;
XX
XX 15-APR-2004 (first entry)
DT
XX ECMCAD protein 55022490CD1.
DE
XX
KW nootropic; antisickling; antianemic; antitumor; anti-HIV; antiallergic;
KW antianemic; antiasthmatic; immunosuppressive; antiatherosclerotic;
KW dermatological; nephrotrophic; antigout; antithyroid; neuroprotective;
KW osteopathic; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW antiinflammatory; ophthalmological; anticonvulsant; antiparkinsonian;
KW antibacterial; virucide; tranquilizer; neuroleptic; antidiabetic;
KW cyostatic; hepatotropic; gene therapy;
KW human extracellular matrix and cell adhesion molecule; ECMCAD; diagnosis;
KW genetic disorder; adrenoleukodystrophy; Down's syndrome; cystic fibrosis;
KW Gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;
KW Wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;
KW AIDS; adult respiratory distress syndrome; allergy; anemia; asthma;
KW atherosclerosis; autoimmune hemolytic anemia; contact dermatitis;
KW Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;
KW osteoporosis; psoriasis; rheumatoid arthritis; scleroderma;
KW systemic lupus erythematosus; ulcerative colitis; uveitis;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; multiple sclerosis;
KW meningitis; periodic paralysis; mental disorder; mood; anxiety;
KW schizophrenia; amnesia; diabetic neuropathy; connective tissue disorder;
KW osteoporosis; Paget's disease; osteonecrosis; osteomyelitis;
KW chondrosarcoma; giant cell tumor; psoriatic arthritis;
KW infectious arthritis; systemic sclerosis; cell proliferative disorder;
KW actinic keratosis; atherosclerosis; hepatitis; psoriasis; cancer;

adenocarcinoma; leukemia; lymphoma; melanoma; myeloma.

Homo sapiens.

WO200202634-A2.

10-JAN-2002.

29-JUN-2001; 2001WO-US021067.

30-JUN-2000; 2000US-0215454P.

18-JUL-2000; 2000US-0219462P.

12-OCT-2000; 2000US-0240106P.

12-OCT-2000; 2000US-0240111P.

27-OCT-2000; 2000US-0244021P.

14-NOV-2000; 2000US-0248887P.

16-NOV-2000; 2000US-0249570P.

(INCY-) INCYTE GENOMICS INC.

Tang YT, Yue H, Azimzai Y, He A, Batra S, Lo TP, Nguyen DB; Burrill JD, Marcus GA, Zingler KA, Gandhi AR, Lal P, Kearney L; Burford N, Yao MG, Walla NK, Elliot VS, Patterson C, Khan FA; Baughn MR, Hafalia AJA, Policky JL, Au-Young J, Lu Y, Borowsky ML; Lu DAM, Ramkumar J, Yang J, Gururajan R, Warren BA, Gietzen K; Xu Y, Kallick DA, Lee EA, Thangavelu K, Delegeane AM, Lee S;

WPI; 2002-154732/20.

N-PSDB; ADI28067.

Novel isolated human extracellular matrix and cell adhesion molecules useful for treating, preventing connective tissue disorder e.g. osteoporosis. Paget's disease, genetic disorder e.g. cystic fibrosis, thalassemia.

Claim 1; SEQ ID NO 23; 270pp; English.

The invention relates to a novel isolated human extracellular matrix and cell adhesion molecule (referred to as ECMCAD 1-36), its biologically active or immunogenic fragment or a sequence comprising 90 % identity to ECMCAD 1-36. The molecule is useful for screening a compound for effectiveness as agonist or antagonist of itself. The protein and its encoding nucleic acid are useful in the diagnosis, treatment and prevention of genetic disorder such as adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's disease, myotonic dystrophy, sickle cell anemia, thalassemia, Wilms' tumor, etc, immunological disorders such as acquired immunodeficiency syndrome (AIDS), adult respiratory distress syndrome, allergies, anemia, asthma, atherosclerosis, psoriasis, rheumatoid hemolytic anemia, contact dermatitis, Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoporosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, ulcerative colitis, uveitis, etc, a neurological disorder such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease, multiple sclerosis, bacterial and viral meningitis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, amnesia, diabetic neuropathy, etc, connective tissue disorder such as osteoporosis, Paget's disease, osteonecrosis, osteomyelitis, chondrosarcoma, giant cell tumor, psoriatic arthritis, infectious arthritis, systemic sclerosis, etc, and a cell proliferative disorder such as actinic keratosis, atherosclerosis, hepatitis, psoriasis, cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, etc. This sequence represents one of the novel proteins.

Sequence 1255 AA;

Query Match 90.3%; Score 56; DB 5; Length 1255;

Best Local Similarity 66.7%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WSXWSXCSXXCG 12

113 WSAWSICSRSCG 124

RESULT 14

ADO29008

ID ADO29008 standard; protein; 1515 AA.

XX ADO29008;

XX 29-JUL-2004 (first entry)

XX Mouse novel GPCR BAI3, SEQ ID NO:107.

G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytotstatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic; CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic; virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antiulcer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse; murine; receptor.

OS Mus musculus.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F; PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

XX N-PSDB; ADO29009.

Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 1; SEQ ID NO 107; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g.,

CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 1515 AA;

Query Match 90.3%; Score 56; DB 8; Length 1515;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 297 WSQWSACSVTCG 308

RESULT 15

AAW99302
ID AAW99302 standard; protein; 1522 AA.

XX AC AAW99302;

DT 21-MAY-1999 (first entry)

XX DE Human BAI3 protein.

XX KW Human; BAI3; brain; cancer; drug; diagnosis; prevention; treatment.

XX OS Homo sapiens.

XX PN JP11032766-A.

XX PD 09-FEB-1999.

XX PF 16-JUN-1997; 97JP-00176485.

XX PR 23-MAY-1997; 97JP-00150460.

XX (SAKA) OTSUKA PHARM CO LTD.

XX DR WPI; 1999-183823/16.

XX DR N-PSDB; AAX21357.

XX PT New human BAI gene - is expressed in brain plays important role in cancer
formation.

XX PS Claim 2; Page 26-30; 62pp; Japanese.

XX CC This sequence represents the human BAI3 protein. The gene is expressed
specifically in the brain and plays an important role in cancer formation
in the brain. The BAI3 protein can be used in drug compositions to
diagnose, prevent or treat such cancers

SQ Sequence 1522 AA;

Query Match 90.3%; Score 56; DB 2; Length 1522;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WSXWSXCSXXCG 12
||| ||| |||
Db 297 WSQWSACSVTCG 308

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